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095Y35
ID Q95Y35 PRELIMINARY; PRT; 327 AA.
AC Q95Y35;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEORETICAL 38.2 KDA PROTEIN.
GN Y108G3AL.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Courtney L.;
RT "The sequence of C. elegans cosmid Y108G3AL.";
RL submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission";
RL submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AC024744; AAK72068.1; -.
KW Hypothetical protein.
SQ SEQUENCE 327 AA; 38186 MW; ASE291465E1BCF67 CRC64;

Query Match 84.8%; Score 28; DB 5; Length 327;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 144 FTLKISR 150

RESULT 14
Q9CUI6 PRELIMINARY; PRT; 346 AA.
AC Q9CUI6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 1110021E09R1X PROTEIN (FRAGMENT).
GN 1110021E09R1X.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

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RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seyer T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsunk S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL, AK015938; BAB30042.1; -.
DR MGD; MGI:1914171; 1110021E09R1X.
FT NON_TER 346
SQ SEQUENCE 346 AA; 39909 MW; FFCBC8EF7A90DE95 CRC64;

Query Match 84.8%; Score 28; DB 11; Length 346;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 137 FTLKISR 143

RESULT 15
Q93XF8 PRELIMINARY; PRT; 347 AA.
AC Q93XF8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE KINESIN HEAVY CHAIN (FRAGMENT).
GN KIN6.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Poaceae; Andropogoneae; Zea.
OX NCBI_TaxId=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE KERNELS;
RA Lawrence C.J., Malberg R.L., Muszynski M.G., Dawe R.K.;
RT "Maximum likelihood methods reveal conservation of function among
RL closely related kinesin families.";
DR J. Mol. Evol. 0:0-0(2001).
DR EMBL, AF272754; AAK91817.1; -.
FT NON_TER 1
SQ SEQUENCE 347 AA; 37914 MW; 889AEEF07B56F62BA CRC64;

QY 1 FTLKIS 6
DB 221 FTLKIS 226

Search completed: July 15, 2002, 13:22:46
Job time: 1482 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 12:57:57 : Search time 228.39 Seconds
(without alignments)
3.404 Million cell updates/sec

Title: US-09-712-819A-6

Sequence: 33
1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.GeneSeq_032802:*
1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
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22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	32	19	AAW79207
2	33	100.0	32	22	AA86295
3	33	100.0	81	17	AA89294
4	33	100.0	89	16	AA88082
5	33	100.0	92	13	AA827009
6	33	100.0	93	21	AA56670
7	33	100.0	100	16	AA872067
8	33	100.0	100	16	AA872066
9	33	100.0	100	22	AA812271
10	33	100.0	100	22	AA806958
11	33	100.0	100	22	AA806959

12	33	100.0	100	22	AA806960
13	33	100.0	100	22	AA806961
14	33	100.0	100	22	AA806962
15	33	100.0	100	22	AA806963
16	33	100.0	100	22	AA806964
17	33	100.0	100	22	AA806965
18	33	100.0	100	22	AA806966
19	33	100.0	100	22	AA806967
20	33	100.0	101	14	AA836529
21	33	100.0	104	18	AA804600
22	33	100.0	106	22	AB843489
23	33	100.0	106	22	AB826451
24	33	100.0	106	22	AA864423
25	33	100.0	106	22	AA877235
26	33	100.0	106	22	AA821171
27	33	100.0	106	22	AA837382
28	33	100.0	108	14	AA838594
29	33	100.0	108	19	AA858494
30	33	100.0	109	20	AA839809
31	33	100.0	110	14	AA838159
32	33	100.0	110	22	AA877590
33	33	100.0	111	13	AA824808
34	33	100.0	111	14	AA842803
35	33	100.0	111	17	AA899849
36	33	100.0	111	21	AA895225
37	33	100.0	111	21	AA895227
38	33	100.0	111	22	AA806948
39	33	100.0	111	22	AA806996
40	33	100.0	112	14	AA832239
41	33	100.0	112	15	AA852058
42	33	100.0	112	16	AA882961
43	33	100.0	112	16	AA868741
44	33	100.0	112	16	AA879248
45	33	100.0	112	17	AA895217

ALIGNMENTS

RESULT 1	
AAW79207	standard; Protein; 32 AA.
ID	AAW79207
AC	AAW79207;
DT	21-DEC-1998 (first entry)
DE	Framework 3 region of human V kappa gene HUM5400.
XX	
XX	Monoclonal antibody; MAb; LO-CD2a; humanised antibody; CD2 antigen;
KW	human lymphocyte; immune response; chimeric; graft-versus-host disease;
KW	T-cell; transplant rejection; autoimmune disease; HUM5400.
OS	Homo sapiens.
PN	US5817311-A.
XX	
PD	06-OCT-1998.
XX	
PF	07-JUN-1995; 95US-0472281.
XX	
PR	07-JUN-1995; 95US-0472281.
PR	05-MAR-1993; 93US-0027008.
PR	09-SEP-1993; 93US-0119032.
PR	29-MAR-1995; 95US-0407009.
XX	
PA	(UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX	
PI	Bazin H, Latine D;
XX	
DR	WPI; 1998-556337/47.
XX	
PT	Inhibition of T-cell mediated immune response with anti-CD2

Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Light chain variab
Anti-DNA antibody
Peptide #10995 enc
Protein #8450 enc
Human Dran expres
Human bone marrow
Peptide #7605 enco
Peptide #1419 enc
Human lambda light
Human kappa light
TRL 6 antibody lig
Sequence of the 11
Human bone marrow
RSV19 light chain
Murine antibody 58
Anti-platelet glyc
Anti-platelet glyc
Human HP-21/28 kap
Human kappa light
Humanised MAb ligh
Light chain variab
Antibody 38193 lig
Mab B3 light chain
Light chain variab
B3 immunoglobulin

PT	monoclonal antibody LO-CD2a - used for preventing transplant
PT	rejection or for treating graft-versus-host disease or auto-immune
PT	diseases
XX	
XX	
PS	Example 7: Columns 33-34; 96pp; English.
XX	
CC	This represents the amino acid sequence of the framework 3 region of
CC	human V kappa gene HUM5400. This is used to construct a humanised antibody
CC	LO-CD2a. LO-CD2a relates to the use of the monoclonal antibody
CC	(Mab) LO-CD2a or a humanised or a chimeric version of the LO-CD2a
CC	antibody for the inhibition of a T-cell mediated immune response in a
CC	patient. The Mab LO-CD2a (produced by hybridoma cell line ATCC HB 11423)
CC	can bind to an epitope on the CD2 antigen of the human lymphocytes. The
CC	T-cell mediated immune response in a patient can be inhibited by
CC	administering the Mab LO-CD2a or an antibody that binds to the same
CC	human lymphocyte epitope as LO-CD2a. The method is used for preventing
CC	transplant rejection or for treating graft-versus-host disease or for
CC	treating autoimmune diseases.
XX	
XQ	Sequence 32 AA:

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Query Match      100.0%; Score 33; DB 19; length 32;
Best local Similarity 100.0%; Pred. NO. 1.3;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy	1	FTLKISR	7
Db	15	ftlkisr	21

RESULT	2
AAB86295	
ID	AAB86295 standard; peptide: 32 AA.

DT 13-SEP-2001 (first entry)

Murine derived anti-body wue-1 light chain variable region FW-3.

KW antibody; wue-1; variable region; light chain; heavy chain; antitumor immunomodulatory; cognate antigen identification; autoimmune disease; tumor; multiple myeloma; lymphoma; plasmocytoma; FW-3.

OS Mus sp.

PN DE19962583-A1.

PD 28-JUN-2001.

PF 23-DEC-1999; 99DE-1062583.

PR 23-DEC-1999; 99DE-1062583.

PA (MUEL/) MUELLER-HERMELINK H K.
PA /CBET/) CBETNER A

PI mueller-Hermelink HK, Greiner A;

DR WPI; 2001-426596/46.

PT New antibodies specific for plasma cells, useful for treatment and
 PT diagnosis of autoimmune diseases and plasma cell tumors -
 XX
 PS Claim 1; Page 10; 18pp: German

This invention describes novel antibodies (Ab) in which the variable region (VR) of at least one chain and/or the VR of at least one heavy chain includes at least one of 7 specified sequences, or fragments or these sequences, or contain at least one light chain and/or heavy chain encoded by specific nucleic acid sequences (I) and (II), reproduced, or their fragments. The products of the invention have

CC antitum and immunomodulatory activity. Ab, or other antibodies that
CC recognize the same antigen, are used: (i) to identify cognate antigens;
CC (ii) for specific labeling of plasma cells (PC), for identification or
CC separation, e.g. in an extracorporeal system; (iii) for generating
CC additional antibodies able to label PC; and (iv) for treating autoimmune
CC diseases and/or tumors, e.g. multiple myeloma, lymphoma and/or
CC plasmacytoma. Ab are specific for mature PC, i.e. they do not recognize
CC precursors stages, even though these precursors are used as immunogens. As
CC therapeutic agents, they should show fewer side effects than conventional
CC chemotherapeutic agents. This sequence represents the Wm-1 antibody
CC variable region 1gH chain FW-3 fragment described in the method of the
CC invention.
XX
XX Sequence 32 AA;

Query Match	100.0%	Score 33;	DB 22;	Length 32;
Best Local Similarity	100.0%	Pred. No. 1.3;		
Matches	7;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0

Qy	1	FTLKISR	7
Db	15	ftlkisr	21

```

RESULT      3
AAR92994
ID   AAR92994 standard; Protein; 81 AA

```

DT 18-MAY-1996 (first entry)

Homologous sequences to antibody IOR-R3 variable region light chain.

KM 10R-33 monoclonal antibody; human; mouse; light chain; homology;
KM variable region; epidermal growth factor receptor; hybridoma;
KM framework; cloning; computer; algorithm; immunogenicity;
KM site-directed mutagenesis; T-lymphocyte epitope; tertiary structure;
KM point mutation; antibody engineering; protein engineering;
KM humanised antibody; antitumour; cancer; therapy.

05 Homo sapiens

FH	Key	Location/Qualifiers
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100		

	/note= "Amino acid involved in tertiary structure"
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FT	Region	/note- 24 25	"Amino acid involved in tertiary structure"
FT			

FT	Region	/note- 35-39	"Amino acids involved in tertiary structure
FT	Region	35-39	"Amino acids involved in tertiary structure

Region	Amino acids involved in tertiary structure
FT	46
EI	

FT	Region	/note- amino acid involved in tertiary structure
48		

Region	AMINO acid INVOLVED IN tertiary structure
FT	50.51

Region	FT	7/1000	Involved in cellular structure
53			

FT	Region	71

PN EP699755-A2

PD 06-MAR-1996

PF 27-JUN-1995; 95EP-0201752.
YY

PR 30-JUN-1994; 94CU-0000080.
XX

PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR

XX Mateo de Àcosta del Rio CM, Rodríguez RP, Valladares JL;
PI WPI: 1996-130770/14.
XX
XX
PT Identifying interspecies differences in amino acid sequence of Ig
PT T-cell epitopes - by sequence comparison, also humanised antibodies
PT contg. altered T-cell epitopes, retaining antigen specificity but
XX not immunogenicity, esp. for tumour treatment
XX
PS Claim 14; Fig 3; 33pp; English.
XX
CC The sequence represents residues from a human immunoglobulin with
CC homology to the light chain variable region from monoclonal antibody
CC 10R-83 (AAR92993), specific for epidermal growth factor receptor,
CC produced by a mouse hybridoma. The sequence is partial, and
CC complementarity determining regions are omitted. The sequence is
CC isolated by comparison of human and mouse immunoglobulins and
CC analysis for T-lymphocyte antigenic sequences using a computer
CC algorithm. Residues not within a complementarity determining region,
CC canonical structure or Verneier zone may be modified to reduce
CC immunogenicity in humans (e.g. in sequence AAR92995). This method,
CC which involves the introduction of only a few point mutations into
CC T-cell epitope coding regions, is generally applicable in humanisation
CC of mouse antibodies. The resulting humanised antibodies may be used
CC e.g. as antitumour agents. They retain the antigen recognition of the
CC original antibody, but are not immunogenic in humans.
XX
SQ Sequence 81 AA;

Query Match 100.0%; Score 33; DB 17; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 53 flikisr 59

RESULT 4
AAR80082
ID AAR80082 standard; Protein; 89 AA.
XX
AC AAR80082;
XX
DT 22-MAY-1996 (first entry)
XX
DE Mouse derived light chain RT3 phage antibody pattern I.
XX
KW Light chain; RT3; murine; catalytic antibody; bacteriophage;
KW pattern I.
XX
XX Mus musculus.
OS
XX
FH Key Location/Qualifiers
FH 1..14
FT /note= "framework region 1"
FT 15..28
FT /note= "complementarity determining region 1"
FT 29..42
FT /note= "framework region 2"
FT 43..49
FT /note= "complementarity determining region 2"
FT 50..82
FT /note= "framework region 3"
FT 83..89
FT /note= "complementarity determining region 3
FT N-terminal fragment"
XX
XX MO9527045-A1.
XX
XX 12-OCT-1995.

XX
XX 30-MAR-1994; 94WO-US03420.
XX
XX
PR 30-MAR-1994; 94WO-US03420.
XX
XX (IGEN-) IGEN INC.
XX
XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
XX Martin MT, McCafferty J, Smith RG, Tiltman RC, Williams RO;
XX WPI: 1995-358624/46.
DR N-PSDB; AAT04629.
XX
XX
PT Production of catalytic antibodies displayed on phage - by
PT generating a gene library of antibody-derived domains and expressing
PT it in phage vectors
XX
PS Disclosure; Fig 10; 133pp; English.
XX
XX AAT04629 encodes AAR80082 mouse derived light chain RT3 phage antibody.
XX The DNA was used in the prepn. of catalytic antibody (CA) producing
XX bacteriophage. The CA can be used to activate/deactivate a
XX biological function in an animal by enhancing the rate of cleavage,
XX or formation of a specific bond within a mol. in vivo.
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 33; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 65 flikisr 71

RESULT 5
AAR27009
ID AAR27009 standard; peptide; 92 AA.
XX
AC AAR27009;
XX
DT 20-MAY-1998 (first entry)
XX
DE Hypercalcaemia agent portion 2.
XX
XX
XX Antihuman parathyroid hormone-related protein; monoclonal antibody;
KW variable region; rodent/human chimeric MAb; constant region; PTNRP.
XX
OS Synthetic.
XX
PN JP04228089-A.
XX
PD 18-AUG-1992.
XX
PF 15-MAY-1991; 91JP-0110565.
XX
PR 15-MAY-1990; 90JP-0124581.
XX
PA (KANF) KANAKA CORP.
XX
DR WPI: 1992-320987/39.
XX
XX
PT Treatment and preventive agent for hypercalcaemia - contg. one of
PT anti-human para-thyroid-hormone-related protein monoclonal antibody,
PT a rodent or chimera monoclonal antibody, fused gene and cell
PT line, etc.
XX
PS Disclosure; Page 13; 18pp; Japanese.
XX
XX The sequences given in AAR27008-11 are fragments which were used in
CC the construction of an agent for the treating and prevention of

CC hypercalcaemia. The agent contained a portion of the antihuman
 CC parathyroid hormone-related protein monoclonal antibody (antihuman
 CC PTHrP Mab). The Mab was used as the active component in the agent.
 CC The agent further comprises a rodent/human chimeric Mab which has a
 CC rodent variable region and a human constant region and recognises
 CC human PTHrP.
 CC
 SQ Sequence 92 AA;

Query Match 100.0%; Score 33; DB 13; Length 92;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
 |||||
 Db 68 ftklkr 74

RESULT 6

AAV56670
 ID AAV56670 standard; protein; 93 AA.

AC AAV56670;

DT 15-FEB-2000 (first entry)

DE Partial peptide fragment of Cynomolgus V kappa cDNA clone 4-5.

KM Complementarity determining region; antibody; primate; immunogenicity;
 KW Old World ape; Old World monkey; antigen-binding affinity.

OS Macaca cynomolgus.

PN WO955369-A1.

PD 04-NOV-1999.

PF 28-APR-1999; 99WO-US09131.

PR 28-APR-1998; 98US-0083367.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PI Taylor AH;

DR WPI: 2000-023265/02.
 N-PSDB: AA239338.

PT Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -

PS Claim 26; Page 101; 123pp; English.

CC The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.
 CC
 SQ Sequence 93 AA;

Query Match 100.0%; Score 33; DB 21; Length 93;

Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7

Db |||||
 76 ftklkr 82

RESULT 7

AA72067
 ID AAR72067 standard; protein; 100 AA.

AC AAR72067;

DT 26-SEP-1995 (first entry)

DE OE7K.7 VK-2 L chain.

KM Graves ophthalmopathy associated immunoglobulin protein;
 KW orbital antigen; monoclonal antibody; light chain; L chain;
 KW variable region; autoimmunity.

OS Homo sapiens.

FT Key Location/Qualifiers
 FT Region 23..38

FT /label= CDR1
 FT Region 54..60

FT /label= CDR2
 FT Region 93..100

FT /label= CDR3

PN WO9508336-A.

PD 30-MAR-1995.

PF 22-SEP-1994; 94WO-US10756.

PR 22-SEP-1993; 93US-0124469.

PA (NICH-) NICHOLS INST DIAGNOSTICS.

PI McLachlan SM, Rapoport B;

DR WPI: 1995-139383/18.
 N-PSDB: AA089326.

PT Graves' ophthalmopathy-associated monoclonal antibody - produced
 PT by molecular cloning of immunoglobulin genes by PCR

PS Claim 4; Page 66; 94pp; English.

CC L- and H-chain DNA was amplified by PCR from Graves' orbital
 CC tissue and clones encoding autoimmune-associated immunoglobulin
 CC fragments were obtained. 14/15 clones of L chain (kappa) regions
 CC showed homology to the putative VK germ-line gene KL012 (given in
 CC AA089317) and the remaining clone, OE7K.7 (AA089326), to the VK005
 CC gene.
 CC
 SQ Sequence 100 AA;

Query Match 100.0%; Score 33; DB 16; Length 100;

Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
 |||||
 Db 76 ftklkr 82

RESULT 8

AA72066
 ID AAR72066 standard; protein; 100 AA.

AC AAR72066;

XX

DT 26-SEP-1995 (first entry)
 XX
 DE VK005 VK region.
 XX
 KW Graves ophthalmopathy associated immunoglobulin protein;
 KW orbital antigen; monoclonal antibody; light chain; L chain;
 KW variable region; autoimmunity.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Region 23..38
 FT /label= CDR1
 FT Region 54..60
 FT /label= CDR2
 FT Region 93..100
 FT /label= CDR3
 XX
 PN WO9508336-A.
 XX
 PD 30-MAR-1995.
 XX
 PF 22-SEP-1994; 94WO-US10756.
 XX
 PR 22-SEP-1993; 93US-0124469.
 XX
 PA (NICH-) NICHOLS INST DIAGNOSTICS.
 XX
 PI McLachlan SM, Rapoport B;
 XX
 DR WPT. 1995-139383/18.
 DR N-PSDB; AA089325.
 XX
 PT Graves' ophthalmopathy-associated monoclonal antibody - produced
 PT by molecular cloning of immunoglobulin genes by PCR
 XX
 PS Disclosure: Page 67; 94pp; English.
 XX
 CC L- and H-chain DNA was amplified by PCR from Graves' orbital
 CC tissue and clones encoding autoimmune-associated immunoglobulin
 CC fragments were obtained. 14/15 clones of L chain (kappa) regions
 CC showed homology to the putative VK germline gene K1012 (given in
 CC AA089317) and the remaining clone, OF7K.7 (AA089326), to the VK005
 CC gene.
 XX
 SQ Sequence 100 AA;
 XX

Query Match 100.0%; Score 33; DB 16; Length 100;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 FTIKISR 7
 |||||
 Db 76 ftklksr 82

RESULT 9
 AAE12711
 ID AAE12711 standard; peptide; 100 AA.
 XX
 AC AAE12711;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Antibody variable light chain region (VL) from DP47 germ line.
 XX
 KW Tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;
 KW variable light chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy.
 XX
 OS Unidentified.
 XX

PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx WFG;
 XX
 DR WPI. 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1-binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1
 XX
 PS Example 1; Page 35; 126pp; English.
 XX
 CC The invention relates to an isolated tumor-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is antibody variable light chain
 CC region (VL) from DP47 germ line.
 XX
 SQ Sequence 100 AA;
 XX

Query Match 100.0%; Score 33; DB 22; Length 100;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 FTIKISR 7
 |||||
 Db 76 ftklksr 82

RESULT 10
 AAE06958
 ID AAE06958 standard; protein; 100 AA.
 XX
 AC AAE06958;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Murine 1D9 antibody partial kappa light chain variable (VK) region.
 XX
 KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody;
 KW neointimal hyperplasia; VK; kappa light chain variable region.
 XX
 OS Mus sp.
 XX
 PN WO200157226-A1.

XX 09-AUG-2001.
 PD
 XX 02-FEB-2001; 2001WO-US03537.
 PF
 XX 03-FEB-2000; 2000US-0497625.
 PR
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX WPI; 2001-488888/53.
 DR
 XX Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT -
 XX
 PS Disclosure; Fig 13; 183pp; English.
 XX
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is murine 1D9 antibody partial kappa light chain
 CC variable (VK) region.
 CC
 XX
 SQ Sequence 100 AA;
 QY
 Query Match 100.0%; Score 33; DB 22; Length 100;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 |||||
 Db 76 fllklisr 82
 RESULT 11
 AAE06959
 ID AAE06959 standard; Protein: 100 AA.
 XX
 AC AAE06959;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Mouse germline kappa light chain variable (VK) region, 70/3.
 XX
 KW Mouse: humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;

KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VK; kappa light chain variable region.
 XX
 OS Mus sp.
 XX
 PN WO200157226-A1.
 XX
 PD 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-US03537.
 XX
 PR 03-FEB-2000; 2000US-0497625.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX WPI; 2001-488888/53.
 DR
 XX Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT -
 XX
 PS Disclosure; Page 147; 183pp; English.
 XX
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is mouse germline kappa light chain variable
 CC (VK) region, 70/3.
 CC
 XX
 SQ Sequence 100 AA;
 QY
 Query Match 100.0%; Score 33; DB 22; Length 100;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 |||||
 Db 76 fllklisr 82
 RESULT 12
 AAE06960
 ID AAE06960 standard; Protein: 100 AA.
 XX
 AC AAE06960;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Mouse germline kappa light chain variable (VK) region, 70/1.
 XX
 KW Mouse: humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;

KM neuroprotective; immunosuppressive; human immunodeficiency virus;
 KM HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KM inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KM multiple sclerosis; atherosclerosis; restenosis; asthma;
 KM anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KM fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KM AIDS; inflammatory glomerulopathy; vascular intervention;
 KM neointimal hyperplasia; VK; kappa light chain variable region.
 OS Mus sp.
 XX WO200157226-A1.
 XX PD 09-AUG-2001.
 XX PF 02-FEB-2001; 2001WO-US03537.
 XX PR 03-FEB-2000; 2000US-0497625.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX DR WPI: 2001-488888/53.
 XX PT Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT -
 XX PS Disclosure: Page 148; 183pp; English.
 XX CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising a portion of an immunoglobulin of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherosclerosis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IGE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is mouse germline kappa light chain variable
 CC (VK) region, 70/1.
 CC XX
 CC Sequence 100 AA:
 CC SQ
 CC
 CC Query Match 100.0%; Score 33; DB 22; Length 100;
 CC Best Local Similarity 100.0%; Pred. No. 4;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC OY 1 FTLKISR 7
 CC |1111111
 CC Db 76 ftlkisr 82
 CC
 CC RESULT 13
 CC AAE06961
 CC ID AAE06961 standard: Protein: 100 AA.
 CC XX
 CC AC AAE06961:

XX 16-OCT-2001 (first entry)
 XX DE Mouse germline kappa light chain variable (VK) region, 70/2.
 XX
 XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 XX neuroprotective; immunosuppressive; human immunodeficiency virus;
 XX HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 XX inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 XX multiple sclerosis; atherosclerosis; restenosis; asthma;
 XX anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 XX fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 XX AIDS; inflammatory glomerulopathy; vascular intervention;
 XX neointimal hyperplasia; VK; kappa light chain variable region.
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 XX Misc-difference 7
 XX FT label=Unknown
 XX FT
 XX
 XX WO200157226-A1.
 XX PD 09-AUG-2001.
 XX PF 02-FEB-2001; 2001WO-US03537.
 XX PR 03-FEB-2000; 2000US-0497625.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX DR WPI: 2001-488888/53.
 XX PT Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT -
 XX PS Disclosure: Page 148; 183pp; English.
 XX CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising a portion of an immunoglobulin of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as Rheumatoid
 CC arthritis and multiple sclerosis, atherosclerosis and atherosclerosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IGE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is mouse germline kappa light chain variable
 CC (VK) region, 70/2.
 CC XX
 CC Sequence 100 AA:
 CC SQ
 CC
 CC Query Match 100.0%; Score 33; DB 22; Length 100;
 CC Best Local Similarity 100.0%; Pred. No. 4;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC

QY	1	FTLKISR	7
Db	76	ftlkisr	82

RESULT 14

ID	AAE06962	standard; Protein; 100 AA.

AC AAE06962;

DT 16-OCT-2001 (first entry)

DE Mouse germline kappa light chain variable (VK) region, V-IB.

KM Mouse; huminised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KM neuroprotective; immunosuppressive; human immunodeficiency virus;
KM HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KM inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock
KM multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KM anaplastic malignancy; inflammation; stenosis; allograft rejection;
KM fibrotic disease; angioplasty; acquired immune deficiency syndrome;
KM AIDS; inflammatory glomerulopathy; vascular intervention;
KM noncatalytic hyperplasia; VK; kappa; light chain variable region.

OS Mus sp.

PN W0200157226-A1.

PD 09-AUG-2001.

PF 02-FEB-2001; 2001WO-US03537.

PR 03-FEB-2000; 2000US-0497625.

PA (MILL-) MILLENNIUM PHARM INC.

PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

DR WPI; 2001-488888/53.

PT Humanized immunoglobulin for treating a CC-chemokine receptor
PT 2-mediated disorder in a patient, comprises a binding specificity for
PT CCR2, and a non-human antigen binding region and human immunoglobulin

PS Disclosure; Page 148-149; 183pp; English.

The patent discloses a humanised antibody or its antigen-binding fragment having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherosclerosis and arteriosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline kappa light chain variable (Vk) region, V-IB.

SD Sequence 100 AA;

Query Match	100.0%;	Score 33;	DB 22;	Length 100;
Best Local Similarity	100.0%;	Pred. No. 4;		
Matches	7;	Conservative	0;	Mismatches
			0;	Indels
				0;
				Gaps
				0;

QY	1	FTIKISR	7
Db	76	ftlkisr	82

RESULT 15

ID AAE06963 standard; Protein; 100 AA.

AC AAE06963;

DT 16-OCT-2001 (first entry)

DE Mouse germline kappa light chain variable (VK) region, V-IC.

KM Mouse; humanized antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KM neuroprotective; immunosuppressive; human immunodeficiency virus;
KM HIV infection; cytosolic; vasotropic; leukocyte trafficking; allergy;
KM inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock
KM multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KM anaplasia; malignancy; inflammation; stenosis; allograft rejection;
KM fibrotic disease; angioplasty; acquired immune deficiency syndrome;
KM AIDS; inflammatory glomerulopathy; vascular intervention;
KM neonatal hyperplasia; VR; kappa; light chain variable region.

OS Mus sp.

PN W0200157226-A1

PD 09-AUG-2001.

PF 02-FEB-2001; 2001WO-US03537

PR 03-FEB-2000; 2000US-0497625.

PA (MILL-) MILLENNIUM PHARM INC.

PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

DR WPI; 2001-488888/53.

Humanized immunoglobulin for treating a CC-chemokine receptor
 2-mediated disorder in a patient, comprises a binding specificity for
 3CCR2, and a non-human antigen binding region and human immunoglobulin
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Disclosure; Page 149; 183pp; English.

The patent discloses a humanized antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanized antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating of HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis and in the manufacture of a medicament for treating CCR2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanized antibodies are also useful for inhibiting narrowing of the

CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
CC a vessel in a mammal, preferably associated with vascular intervention.
CC The present sequence is mouse germline kappa light chain variable
CC (VK) region, V-IC.
XX
SQ Sequence 100 AA;

Query Match 100.0%; Score 33; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||
Db 76 flIKISR 82

Search completed: July 15, 2002, 12:57:58
Job time: 414 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:59:18 ; Search time 75.67 Seconds
(without alignments)
2.260 Million cell updates/sec

Title: US-09-712-819A-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	32	1	US-08-477-877B-33 Sequence 33, Appl
2	33	100.0	32	1	US-07-977-696C-71 Sequence 71, Appl
3	33	100.0	32	1	US-08-129-930B-71 Sequence 71, Appl
4	33	100.0	32	2	US-08-472-281A-33 Sequence 33, Appl
5	33	100.0	32	2	US-08-477-989B-33 Sequence 33, Appl
6	33	100.0	32	4	US-08-976-288A-71 Sequence 71, Appl
7	33	100.0	81	1	US-08-497-312-19 Sequence 19, Appl
8	33	100.0	104	3	US-08-881-037-37 Sequence 37, Appl
9	33	100.0	108	1	US-08-488-113B-151 Sequence 151, App
10	33	100.0	108	1	US-08-477-484B-151 Sequence 151, App
11	33	100.0	108	1	US-08-107-669D-15 Sequence 15, Appl
12	33	100.0	108	1	US-08-472-788A-15 Sequence 15, Appl
13	33	100.0	108	2	US-08-477-531B-15 Sequence 15, Appl
14	33	100.0	108	2	US-08-646-360-151 Sequence 151, App
15	33	100.0	108	2	US-08-082-842A-15 Sequence 15, Appl
16	33	100.0	108	2	US-08-378-939-22 Sequence 22, Appl
17	33	100.0	108	2	US-08-378-939-28 Sequence 28, Appl
18	33	100.0	108	2	US-08-378-939-30 Sequence 30, Appl
19	33	100.0	108	4	US-08-839-765-151 Sequence 151, App
20	33	100.0	108	4	US-09-136-389-151 Sequence 151, App
21	33	100.0	110	1	US-08-244-626-2 Sequence 2, Appl1
22	33	100.0	111	1	US-07-942-245-29 Sequence 29, Appl
23	33	100.0	112	1	US-08-053-171-15 Sequence 15, Appl
24	33	100.0	112	1	US-08-053-171-16 Sequence 16, Appl
25	33	100.0	112	1	US-08-331-398A-48 Sequence 48, Appl
26	33	100.0	112	1	US-08-331-398A-49 Sequence 49, Appl
27	33	100.0	112	1	US-08-331-398A-50 Sequence 50, Appl

28	33	100.0	112	1	US-07-942-245-28 Sequence 28, Appl
29	33	100.0	112	1	US-08-478-039-88 Sequence 88, Appl
30	33	100.0	112	1	US-08-478-039-89 Sequence 89, Appl
31	33	100.0	112	1	US-08-477-877B-89 Sequence 89, Appl
32	33	100.0	112	1	US-08-077-252B-3 Sequence 3, Appl1
33	33	100.0	112	1	US-08-476-349A-88 Sequence 88, Appl
34	33	100.0	112	1	US-08-476-349A-89 Sequence 89, Appl
35	33	100.0	112	1	US-08-388-672A-25 Sequence 25, Appl
36	33	100.0	112	2	US-08-475-000-18 Sequence 18, Appl
37	33	100.0	112	2	US-08-472-281A-89 Sequence 89, Appl
38	33	100.0	112	2	US-08-483-199-18 Sequence 18, Appl
39	33	100.0	112	2	US-08-859-649-19 Sequence 19, Appl
40	33	100.0	112	2	US-08-859-649-29 Sequence 29, Appl
41	33	100.0	112	2	US-08-606-293-4 Sequence 4, Appl1
42	33	100.0	112	2	US-08-606-293-8 Sequence 8, Appl1
43	33	100.0	112	2	US-08-678-194-6 Sequence 6, Appl1
44	33	100.0	112	2	US-08-752-844-15 Sequence 15, Appl
45	33	100.0	112	2	US-08-484-508-18 Sequence 18, Appl

ALIGNMENTS

```
RESULT 1
US-08-477-877B-33
; Sequence 33, Application US/08477877B
; Patent No. 5730979
;
; GENERAL INFORMATION:
; APPLICANT: Bazzin, Herv
; APPLICANT: Latine, Dominique
; TITLE OF INVENTION: LO-CC2a Antibody and Uses thereof for Inhibiting T-Cell Act
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Giffillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; US-08-477-877B-33
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Query Match 100.0%: Score 33; DB 1; Length 32;
Best Local Similarity 100.0%: Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
| | | | |
DB 15 FTLKISR 21

RESULT 2
US-07-977-696C-71

; Sequence 71, Application US/07977696C
; Patent No. 5792852

; GENERAL INFORMATION:

; APPLICANT: do Couto, Fernando J.R.

; APPLICANT: Ceriani Dr., Roberto L.

; APPLICANT: Peterson Dr., Jerry A.

; APPLICANT: Padlan Dr., Eduardo A.

; TITLE OF INVENTION: Analogue Peptides with Specificity

; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI

; STREET: 444 South Flower Street, Suite 2000

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/977,696C

; FILING DATE: 11-16-92

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Amzel Ph.D., Viviana

; REGISTRATION NUMBER: 30,930

; REFERENCE/DOCKET NUMBER: P66 38227

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 748-6868

; TELEFAX: (510) 748-6868

; TELEX: n.a.

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 32 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-977-696C-71

Query Match 100.0%: Score 33; DB 1; Length 32;
Best Local Similarity 100.0%: Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
| | | | |
DB 15 FTLKISR 21

RESULT 3
US-08-129-930B-71

; Sequence 71, Application US/08129930B
; Patent No. 5804187

; GENERAL INFORMATION:

; APPLICANT: do Couto Dr., Fernando J.R.

; APPLICANT: Ceriani Dr., Roberto L.

; APPLICANT: Peterson Dr., Jerry A.

; APPLICANT: Padlan Dr., Eduardo A.

; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: V. AMZEL & ASSOC.

; STREET: 2055 No. 5804187th Broadway, Suite 201

; CITY: Walnut Creek

; STATE: California

; COUNTRY: USA

; ZIP: 94596

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/129,930B

; FILING DATE: September 30, 1993

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Amzel Ph.D., Viviana

; REGISTRATION NUMBER: 30,930

; REFERENCE/DOCKET NUMBER: CRPC-008A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 521-1333

; TELEFAX: (510) 521-3541

; TELEX: n.a.

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 32 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-129-930B-71

Query Match 100.0%: Score 33; DB 1; Length 32;
Best Local Similarity 100.0%: Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
| | | | |
DB 15 FTLKISR 21

RESULT 4
US-08-472-281A-33

; Sequence 33, Application US/08472281A
; Patent No. 5817311

; GENERAL INFORMATION:

; APPLICANT: Bazin, Herv

; APPLICANT: latine, Dominique

; TITLE OF INVENTION: Lb-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act

; NUMBER OF SEQUENCES: 96

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cecchi, Stewart & Olstein

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,281A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oistein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-472-281A-33

Query Match 100.0%; Score 33; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
|||||||
DB 15 FTLKISR 21

RESULT 5
US-08-477-989B-33
Sequence 33, Application US/08477989B
Patent No. 5951983
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latine, Dominique
APPLICANT: Kaplan, Ruth
APPLICANT: Kieher-Emmons, Thomas
APPLICANT: Postema, Christina E.
APPLICANT: White-Schaff, Mary
TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bahn, Gillfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,989B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Oistein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-477-989B-33

Query Match 100.0%; Score 33; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
|||||||
DB 15 FTLKISR 21

RESULT 6
US-08-976-288A-71
Sequence 71, Application US/08976288A
Patent No. 6315997
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Klt and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretly, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-71

Query Match 100.0%; Score 33; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||||
DB 15 FTLKISR 21

RESULT 7
US-08-497-312-19
Sequence 19, Application US/08497312
Patent No. 5712120
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for obtaining modified
TITLE OF INVENTION: Immunoglobulins with reduced immunogenicity of murine
TITLE OF INVENTION: antibody variable domains, compositions containing them.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 y 15, ATABEY PLATA
CITY: HAVANA
STATE:
COUNTRY: CUBA
ZIP: 11600
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPC)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 262905
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801/531-9168
TELEFAX: 388961 1PM04UT
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-497-312-19

Query Match 100.0%; Score 33; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||||
DB 53 FTLKISR 59

RESULT 8
US-08-881-037-37

Sequence 37, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5560
TELEFAX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-37

Query Match 100.0%; Score 33; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||||
DB 68 FTLKISR 74

RESULT 9
US-08-488-113B-151
Sequence 151, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studilka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-488-113B-151

Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
Db 72 FTLKISR 78

RESULT 10
US-08-477-484B-151
Sequence 151, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-477-484B-151

Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
Db 72 FTLKISR 78

RESULT 11
US-08-107-669D-15
Sequence 15, Application US/08107669D
Patent No. 5766866
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D
FILING DATE: 13-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991

```
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2500
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-669D-15

Query Match      100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 72 FTLKISR 78

RESULT 12
US-08-472-788A-15
Sequence 15, Application US/08472788A
Patent No. 5770196
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,788A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-788A-15

Query Match      100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 72 FTLKISR 78

RESULT 13
US-08-477-531B-15
Sequence 15, Application US/08477531B
Patent No. 5821123
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,531B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2540
TELEFAX: 202/371-2600
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-531B-15

Query Match      100.0%; Score 33; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 72 FTLKISR 78

RESULT 14
US-08-646-360-151
Sequence 151, Application US/08646360
Patent No. 5837491
```

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-646-360-151

Query Match 100.0%; Score 33; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
DB 72 FTLKISR 78

RESULT 15
US-08-082-842A-15
Sequence 15, Application US/08082842A
Patent No. 5869619
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,842A
FILING DATE: 23-JUN-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimdale, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-842A-15

Query Match 100.0%; Score 33; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
DB 72 FTLKISR 78

Search completed: July 15, 2002, 12:59:19
Job time: 390 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:01:01 ; Search time 95.45 Seconds
(without alignments)
9.060 Million cell updates/sec

Title: US-09-712-819A-7
Perfect score: 43
Sequence: 1 TDFLTRISS 9

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pIR_71:*
2: pIR1:*
3: pIR3:*
4: pIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	54	2 JT0521	Ig kappa chain V-I
2	43	100.0	71	2 S21526	Ig kappa chain V r
3	43	100.0	78	2 S34102	Ig kappa chain V r
4	43	100.0	79	2 S24215	Ig kappa chain - m
5	43	100.0	81	2 PH1048	Ig light chain V r
6	43	100.0	86	2 S16826	Ig kappa chain V r
7	43	100.0	86	2 S16834	Ig kappa chain V r
8	43	100.0	86	2 S16836	Ig kappa chain V r
9	43	100.0	86	2 S34086	Ig kappa chain V r
10	43	100.0	86	2 S16840	Ig kappa chain V r
11	43	100.0	86	2 S16837	Ig kappa chain V r
12	43	100.0	86	2 S16833	Ig kappa chain V-I
13	43	100.0	86	2 S16830	Ig kappa chain V r
14	43	100.0	86	2 S16824	Ig kappa chain V r
15	43	100.0	86	2 S16829	Ig kappa chain V r
16	43	100.0	87	2 S34084	Ig kappa chain V r
17	43	100.0	87	2 S34083	Ig kappa chain V r
18	43	100.0	88	2 S21528	Ig kappa chain V r
19	43	100.0	88	2 S21525	Ig kappa chain V r
20	43	100.0	88	2 S21522	Ig kappa chain V r
21	43	100.0	91	2 PH1071	Ig kappa chain V r
22	43	100.0	91	2 S37521	Ig kappa chain V r
23	43	100.0	92	2 S37533	Ig kappa chain V r
24	43	100.0	92	2 S37530	Ig kappa chain V r
25	43	100.0	92	2 S37529	Ig kappa chain V r
26	43	100.0	92	2 S37535	Ig kappa chain V r
27	43	100.0	92	2 S37512	Ig kappa chain V r
28	43	100.0	92	2 S37531	Ig kappa chain V r
29	43	100.0	92	2 S37534	Ig kappa chain V r

30	43	100.0	92	2 S37532	Ig kappa chain V r
31	43	100.0	92	2 S37516	Ig kappa chain V r
32	43	100.0	92	2 S37522	Ig kappa chain V r
33	43	100.0	92	2 S37506	Ig kappa chain V r
34	43	100.0	92	2 S37504	Ig kappa chain V r
35	43	100.0	94	2 S20648	Ig heavy chain V r
36	43	100.0	95	2 PH0863	Ig kappa chain V r
37	43	100.0	95	2 PH0867	Ig kappa chain V r
38	43	100.0	96	2 PH1070	Ig light chain V r
39	43	100.0	96	2 G38601	Ig kappa chain V r
40	43	100.0	96	2 S45441	Ig kappa chain V r
41	43	100.0	97	2 A42575	Ig kappa chain V r
42	43	100.0	98	2 PH1066	Ig light chain V r
43	43	100.0	98	2 PH1067	Ig light chain V r
44	43	100.0	98	2 PH1083	Ig light chain V r
45	43	100.0	98	2 S19974	Ig kappa chain V r

ALIGNMENTS

RESULT 1
JT0521
Ig kappa chain V-III region (CPI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 09-May-1997
C:Accession: JT0521
R:Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A:Reference number: JT0511; MUID:89279157
A:Accession: JT0521
A:Molecule type: mRNA
A:Residues: 1-54 <ANK>
A>Note: The sequence shown here is one of eight productive V-D-J mu chain rearrangements
C:Superfamily: Immunoglobulin V region: Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-49/Domain: V region <VRE>
F:50-54/Domain: J region <JRE>

Query Match 100.0%; Score 43; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TDFLTRISS 9
Db 21 TDFLTRISS 29

RESULT 2
S21526
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C:Accession: S34082; S21526
R:Wagner, S.D.; Luzaatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387
A:Accession: S34082
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <MA2>
A:Cross-references: EMBL:X66042; NID:q33318; PIR:CA46841.1; PTD:q33319
C:Superfamily: Immunoglobulin V region: Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 100.0%; Score 43; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
|||||
Db 62 TDFTLTSS 70

RESULT 3

S34102
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C:Accession: S34102
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387
A:Accession: S34102
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78 <WAG>
A:Cross-references: EMBL:X67186
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 43; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
|||||
Db 60 TDFTLTSS 68

RESULT 4

S24215
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24215
R:Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1065-1072, 1991
A:Title: Deletions of immunoglobulin C(kappa) region characterized by the circular excise
A:Reference number: S24214; MUID:91217618
A:Accession: S24215
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-79 <SHI>
A:Cross-references: EMBL:X58202; NID:953718; PID:CAA41178.1; PID:9930195
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 43; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
|||||
Db 42 TDFTLTSS 50

RESULT 5

PH1048
Ig light chain V region (clone 165.49) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1048
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1048
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-81 <TIL>
A:Experimental source: B cell, strain (NZB x NZW)F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 100.0%; Score 43; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
|||||
Db 54 TDFTLTSS 62

RESULT 6

S16826
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16826; S34101
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16826
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54824; NID:933653; PID:CAA38593.1; PID:933654
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distrib
A:Reference number: S34076; MUID:93170387
A:Accession: S34101
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <WAG>
A:Cross-references: EMBL:X67185
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
|||||
Db 60 TDFTLTSS 68

RESULT 7

S16834
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16834
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16834
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54832
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
|||||
DB 60 TDFTLTSS 68

RESULT 8

Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16836
R:Blaisson, G.; Kuntz, J.L.; Pasquall, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737
A:Accession: S16836
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54834
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
|||||
DB 60 TDFTLTSS 68

RESULT 9

Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34086
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387
A:Accession: S34086
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <WAG>
A:Cross-references: EMBL:X67169
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
|||||
DB 62 TDFTLTSS 70

RESULT 10

Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S16840
R:Blaisson, G.; Kuntz, J.L.; Pasquall, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16840
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54838
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
|||||
DB 60 TDFTLTSS 68

RESULT 11

Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16837
R:Blaisson, G.; Kuntz, J.L.; Pasquall, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16837
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54835
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
|||||
DB 60 TDFTLTSS 68

RESULT 12

Ig kappa chain V-III region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16833; S16838
R:Blaisson, G.; Kuntz, J.L.; Pasquall, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16833
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54831
A:Experimental source: clone bkv17
A:Accession: S16838
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>

A:Cross-references: EMBL:X54836
A:Experimental source: clone s1kv14
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTISS 9
|||||
DB 60 TDFTLTISS 68

RESULT 13

S16830
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16830
R:Blaisson, G.; Kuntz, J.L.; Pasquall, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A>Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737
A:Accession: S16830
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54828
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTISS 9
|||||
DB 60 TDFTLTISS 68

RESULT 14

S16824
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16824
R:Blaisson, G.; Kuntz, J.L.; Pasquall, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A>Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737
A:Accession: S16824
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54822
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTISS 9
|||||
DB 60 TDFTLTISS 68

RESULT 15

S16829
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16829
R:Blaisson, G.; Kuntz, J.L.; Pasquall, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A>Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16829
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54827
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTISS 9
|||||
DB 60 TDFTLTISS 68

Search completed: July 15, 2002, 13:01:02
Job time: 468 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:23:33 ; Search time 44.9 Seconds

(without alignments)
7.761 Million cell updates/sec

Title: US-09-712-819a-7

Perfect score: 43

Sequence: 1 TDFPRLTIRSS 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	107	1 KVID_HUMAN	P01596 homo sapien
2	43	100.0	108	1 KVIH_HUMAN	P01600 homo sapien
3	43	100.0	108	1 KVSQ_MOUSE	P01650 mus musculu
4	43	100.0	108	1 KVSQ_MOUSE	P01651 mus musculu
5	43	100.0	108	1 KVSQ_MOUSE	P01652 mus musculu
6	43	100.0	108	1 KVSQ_MOUSE	P01653 mus musculu
7	43	100.0	109	1 KVIH_HUMAN	P01612 homo sapien
8	43	100.0	114	1 KVIH_MOUSE	P01632 mus musculu
9	43	100.0	114	1 KVIH_MOUSE	P01633 mus musculu
10	43	100.0	115	1 KVIH_MOUSE	P01634 mus musculu
11	43	100.0	115	1 KVIH_MOUSE	P01635 mus musculu
12	43	100.0	117	1 KVIH_MOUSE	P01636 mus musculu
13	43	100.0	121	1 KVIH_MOUSE	P01637 mus musculu
14	43	100.0	129	1 KVIH_MOUSE	P01638 mus musculu
15	43	100.0	133	1 KVIH_MOUSE	P01639 mus musculu
16	43	100.0	134	1 KVIH_MOUSE	P01640 mus musculu
17	43	100.0	136	1 KVIH_MOUSE	P01641 mus musculu
18	43	100.0	136	1 KVIH_MOUSE	P01642 mus musculu
19	43	100.0	136	1 KVIH_MOUSE	P01643 mus musculu
20	43	100.0	136	1 KVIH_MOUSE	P01644 mus musculu
21	43	100.0	136	1 KVIH_MOUSE	P01645 mus musculu
22	43	100.0	136	1 KVIH_MOUSE	P01646 mus musculu
23	43	100.0	136	1 KVIH_MOUSE	P01647 mus musculu
24	43	100.0	136	1 KVIH_MOUSE	P01648 mus musculu
25	43	100.0	136	1 KVIH_MOUSE	P01649 mus musculu
26	43	100.0	136	1 KVIH_MOUSE	P01650 mus musculu
27	43	100.0	136	1 KVIH_MOUSE	P01651 mus musculu
28	43	100.0	136	1 KVIH_MOUSE	P01652 mus musculu
29	43	100.0	136	1 KVIH_MOUSE	P01653 mus musculu
30	43	100.0	136	1 KVIH_MOUSE	P01654 mus musculu
31	43	100.0	136	1 KVIH_MOUSE	P01655 mus musculu
32	43	100.0	136	1 KVIH_MOUSE	P01656 mus musculu
33	43	100.0	136	1 KVIH_MOUSE	P01657 mus musculu

34	39	90.7	117	1 KVIH_HUMAN	P01602 homo sapien
35	39	90.7	129	1 KVIH_HUMAN	P18135 homo sapien
36	39	90.7	129	1 KVIH_HUMAN	P18136 homo sapien
37	39	90.7	149	1 KVIH_MOUSE	P01633 mus musculu
38	39	90.7	149	1 KVIH_MOUSE	P01634 mus musculu
39	39	90.7	149	1 KVIH_MOUSE	P01635 mus musculu
40	39	90.7	149	1 KVIH_MOUSE	P01636 mus musculu
41	39	90.7	149	1 KVIH_MOUSE	P01637 mus musculu
42	39	90.7	149	1 KVIH_MOUSE	P01638 mus musculu
43	39	90.7	149	1 KVIH_MOUSE	P01639 mus musculu
44	39	90.7	149	1 KVIH_MOUSE	P01640 mus musculu
45	39	90.7	149	1 KVIH_MOUSE	P01641 mus musculu

ALIGNMENTS

RESULT 1					
ID	KVID_HUMAN	STANDARD:	PRT:	107 AA.	
AC	P01596				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-I region CAR.				
OS	Homo sapiens (Human).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=75075135; PubMed=4216454;				
RA	Milstein C.P., Deverson E.V.,				
RT	*Primary structure of kappa light chain from a human myeloma protein.				
RL	Eur. J. Biochem. 49:377-391(1974).				
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.				
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.				
DR	PIR; A01864; KIHUAR.				
DR	HSSP; P80362; IWTL.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGV_1.				
KW	Immunoglobulin V region; Glycoprotein.				
FT	CARBOHYD 28				
FT	NON_TER 107				
FT	SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;				
QY	1 TDFPRLTIRSS 9				
DB	69 TDFPRLTIRSS 77				
RESULT 2					
ID	KVIH_HUMAN	STANDARD:	PRT:	108 AA.	
AC	P01600				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-I region Hau.				
OS	Homo sapiens (Human).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				

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RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Sevler's 2. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR PIR: A01868; KIH0H0.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003596; I9_V.
DR Pfam: PF00047; I9; 1.
DR SMART: SM00406; IGV; 1.
KM Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
DB 69 TDFLTITSS 77

RESULT 3
KV5Q_MOUSE STANDARD; PRT; 108 AA.
ID KV5Q_MOUSE
AC P01650;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS Ig kappa chain V-V region UPC 61.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INDLIN).
DR PIR: A01929; KVM561.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003596; I9_V.
DR Pfam: PF00047; I9; 1.
DR SMART: SM00406; IGV; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108

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SQ SEQUENCE 108 AA; 11809 MW; FAE4DA36076F2AFE CRC64;

Query Match 100.0%; Score 43; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
DB 69 TDFLTITSS 77

RESULT 4
KV5R_MOUSE STANDARD; PRT; 108 AA.
ID KV5R_MOUSE
AC P01651;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region EPC 109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INDLIN).
DR PIR: B92808; KVM509.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003596; I9_V.
DR Pfam: PF00047; I9; 1.
DR SMART: SM00406; IGV; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11876 MW; 35C116BD60F9310 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
DB 69 TDFLTITSS 77

RESULT 5
KV5S_MOUSE STANDARD; PRT; 108 AA.
ID KV5S_MOUSE
AC P01652;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

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PP	SEQUENCE.
RA	MEDLINE-82099361; PubMed-6798111;
RX	Johnson N., Slankard J., Paul L.;
RT	"The complete V domain amino acid sequences of two myeloma inulin-
RT	binding proteins."
RL	J. Immunol. 128:303-307(1982).
CC	-I. MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC	BIND BETA(2-1)-F-PROCTOPURANOSYL MOIETIES (INULIN).
DR	PIR; A92811; KVM506.
DR	HSSP; P01607; IREI.
DR	InterPro: IPRO03506; Ig_MHC.
DR	InterPro: IPRO03596; Ig_v.
DR	Pfam; Pf00047; Ig; 1.
KV	SMART; SMO0406; IGv; 1.
KV	Immunoglobulin V region.
FT	DOMAIN
FT	1
FT	23
FT	DOMAIN
FT	24
FT	34
FT	DOMAIN
FT	35
FT	49
FT	DOMAIN
FT	50
FT	56
FT	DOMAIN
FT	57
FT	88
FT	DOMAIN
FT	89
FT	97
FT	DOMAIN
FT	98
FT	108
FT	DISULFID
FT	23
FT	88
FT	NON_TER
FT	108
FT	108
QO	SEQUENCE
QO	108 AA; 11810 MW; 8DE4DD31076F2AFB CRC64;
QO	8DE4DD31076F2AFB CRC64;

Query Match	100.0%	Score 43;	DB 1;	Length 108;
Best Local Similarity	100.0%	Pred. No. 0.015;		
Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 TDFITLIS 9			
db	69 TDFITLIS 77			

RESULT	6
ID	KV5T_MOUSE
STANDARD	PRT; 108 AA.
AC	P01653;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	19 kappa Chain V-V region W3082.
OS	Mus musculus (Mouse).
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=82099361; PubMed=6798111;
RA	Johnson N., Slackard J., Paul L., Hood L.;
RT	"The complete V domain amino acid sequences of two myeloma Inlnh-
RT	binding proteins."
RL	J. Immunol. 128:302-307 (1982).
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC	BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
CC	PIR: B92811; KVM82.
DR	HSSP: P80362; IMTL.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; Ig; 1.
DR	SMART: SM00406; IGV; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 23
FT	DOMAIN 24 34
FT	DOMAIN 35 49
FT	DOMAIN 50 56
FT	DOMAIN 57 88
FT	DOMAIN 89 97
FT	DOMAIN 98 108
FT	DISULFID 23 88
FT	NON_TER 108 108
FR	FRAMEWORK-1.
FR	COMPLEMENTARITY-DETERMINING-1.
FR	FRAMEWORK-2.
FR	COMPLEMENTARITY-DETERMINING-2.
FR	FRAMEWORK-3.
FR	COMPLEMENTARITY-DETERMINING-3.
FR	FRAMEWORK-4.
FR	BY SIMILARITY.

SEQ	SEQUENCE	108 AA;	11850 MW;	C50145DC376F30CD	CRC64;
	Query Match		100.0%;	Score 43;	DB 1;
	Best Local Similarity		100.0%;	Pred. No. 0.015;	Length 108;
	Matches	9;	Conservative	0;	Mismatches 0;
					Indels 0;
					Gaps 0;
QY	1 TDFETLTSS	9			
Db	69 TDFETLTSS	77			

RESULT	7			
ID	KVIT_HUMAN	STANDARD;	PRT;	109 AA.
AC	P01612;			
DT	21-JUL-1986 (Rel. 01, Created)			
DR	21-JUL-1986 (Rel. 01, Last sequence update)			
DE	15-JUL-1999 (Rel. 38, Last annotation update)			
OS	Ig kappa chain V-I region Mv.			
OC	Homo sapiens (Human).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
RN	NCBI_TaxID=9606;			
RP	[1]			
RA	SEQUENCE.			
RT	MEDLINE=83081018; PubMed=6816713;			
RL	Eulitz M., Linke R.P.;			
CC	"Primary structure of the variable part of an amyloidogenic Bence-Jones Protein (Mev). An unusual insertion in the third hyper-variable region of a human kappa-immunoglobulin light chain, Hype-Seyler's 2. Physiol. Chem. 363:1347-1358(1982). -I- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO FOUND."			
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN			
DR	PIR: A01879; KIH0WV.			
DR	HSSP: P01730; IWIO.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig_1.			
DR	SMART: SM00406; IgV_1.			
FT	Immunoglobulin V region.			
FT	DOMAIN	1	23	FRAMEWORK-1.
FT	DOMAIN	24	34	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	35	49	FRAMEWORK-2.
FT	DOMAIN	50	56	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	57	88	FRAMEWORK-3.
FT	DOMAIN	89	98	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	99	108	FRAMEWORK-4.
FT	DISULFID	23	88	BY SIMILARITY.
FT	NON_TER	109	109	
SO	SEQUENCE	109 AA;	11870 MW;	B6ABF451D55F5A0 CRC64;

```

Query Match Similarity      100.0%; Score 43; DB 1; Length 109;
Best Local Similarity      100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TDFTLTSS 9
          |||||
Db       69 TDFTLTSS 77

RESULT 8
KVLA_MOUSE STANDARD: PRT; 114 AA.
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE I9 Kappa chain V-I region S107A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=81241357; PubMed=6788890;
RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharif M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
   chains";
RL J. Exp. Med. 153:1366-1370(1981).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U29423; AAC00033.1; -.
DR PIR: A01915; KVM57A.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 40
FT DOMAIN 41 55
FT DOMAIN 56 62
FT DOMAIN 63 94
FT DOMAIN 95 103
FT DOMAIN 104 113
FT DISULFID 23 94
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12717 MW; 32008C8E9DBE67B CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 114;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
DB 75 TDFTLTSS 83

RESULT 9
KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
   subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RP REVISION TO 9.
RA Salomon A.;
CC -1- Submitted (AUG-1996) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR: A01903; K4HULN.

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```

DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 40
FT DOMAIN 41 55
FT DOMAIN 56 62
FT DOMAIN 63 94
FT DOMAIN 95 101
FT DOMAIN 102 113
FT DISULFID 23 94
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 114;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
DB 75 TDFTLTSS 83

RESULT 10
KV31_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1989 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region V6 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
   within the VK locus.";
RL Nucleic Acids Res. 12:929-936(1984).
CC -----
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CC -----
CC EMBL: X01668; -; NOT_ANNOTATED_CDS.
DR PIR: A01900; K3HUVG.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 115
FT DISULFID 43 108
FT NON_TER 115 115

```

SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 115;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
DB 89 TDFTLTSS 97

RESULT 11
KV3J_HUMAN STANDARD; PRT; 116 AA.
AC P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 Kappa chain V-III region VH precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus".
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----
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CC -----
CC EMBL X02725; -; NOT_ANNOTATED_CDS.
DR PTR: A01901; K3HUVH.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 20
FT DOMAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 116;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
DB 90 TDFTLTSS 98

RESULT 12
KV1I_HUMAN STANDARD; PRT; 117 AA.

AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 Kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbits T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RT kappa genes and a pseudogene."
RL Nature 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbits T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
RT recently duplicated human V kappa sequences have diverged by gene
RT conversion."
RL Cell 32:181-189(1983).
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CC -----
CC EMBL K01322; AA58930.1; -;
DR EMBL: K01324; AA58932.1; -;
DR EMBL: V00558; CA23824.1; -;
DR PIR: A01881; K1H011.
DR PIR: A21056; A21056.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 1 22
FT DOMAIN 23 >117 IG KAPPA CHAIN V-I REGION HK101.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12799 MW; D7D0FF3718CE587 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 117;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
DB 91 TDFTLTSS 99

RESULT 13
KV40_HUMAN STANDARD; PRT; 121 AA.
ID KV40_HUMAN
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```

DE Ig kappa chain V-IV region precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combrlato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -1- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
-----
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-----
CC EMBL: 200023; CAA7318.1; -.
DR PIR: A01902; K4HU.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF0047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 1390 MW; 9586AD418BD33974 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 121;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDEFTLTSS 9
DB 95 TDEFTLTSS 103

RESULT 14
ID KY1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrlato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
-----

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-----
CC EMBL: X00965; CAA25477.1; ALT_TERM.
DR PIR: A01883; K1HOWK.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 22
FT SIGNAL 1 22
FT DOMAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 46 56 FRAMEWORK-1.
FT DOMAIN 57 71 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 72 78 FRAMEWORK-2.
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 111 119 FRAMEWORK-3.
FT DOMAIN 120 129 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 45 110 FRAMEWORK-4.
FT NON_TER 129 129 BY SIMILARITY.
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4A8C2F9 CRC64;

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Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 129;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 TDEFTLTSS 9
DB 91 TDEFTLTSS 99

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RESULT 15
ID KY4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combrlato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
-----
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-----
CC EMBL: 200022; CAA7317.1; -.
DR PIR: A01904; K4HUJ1.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.

```

DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 61 75 FRAMEWORK-2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 83 114 FRAMEWORK-3.
 FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 123 132 FRAMEWORK-4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 133 133
 SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
 |||||
 Db 95 TDFTLTSS 103

Search completed: July 15, 2002, 13:23:33
 Job time: 1449 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:22:46 ; Search time 172.49 Seconds

(without alignments)
9.026 Million cell updates/sec

Title: US-09-712-819A-7

Sequence: 43
1 TDFLTTSS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	107	4	Q96SA9 homo sapien
2	43	100.0	107	11	Q9ERZ9 mus musculu
3	43	100.0	108	4	Q9UL77 homo sapien
4	43	100.0	108	4	Q9UL70 homo sapien
5	39	90.7	107	4	Q9UL81 homo sapien
6	39	90.7	108	4	Q9UL83 homo sapien
7	39	90.7	108	4	Q9UL79 homo sapien
8	39	90.7	109	4	Q9UL86 homo sapien
9	39	90.7	109	4	Q9UL85 homo sapien
10	39	90.7	109	4	Q9UL78 homo sapien
11	37	86.0	557	16	Q99XR2 streptococ
12	36	83.7	99	11	Q9UL74 mus musculu
13	35	81.4	116	4	Q96PF6 homo sapien
14	35	81.4	1806	16	Q929J3 listeria in
15	34	79.1	284	12	Q91GM1 kaposi's sa
16	33	76.7	104	11	Q9UL82 mus musculu

17	33	76.7	114	4	Q9UL80 homo sapien
18	33	76.7	233	11	Q91WS9 mus musculu
19	33	76.7	234	11	Q91WF8 mus musculu
20	33	76.7	238	11	Q99M37 mus musculu
21	33	76.7	269	5	Q00814 tritrichomo
22	33	76.7	417	2	Q9RGU3
23	33	76.7	520	16	Q9CM14
24	33	76.7	572	10	Q9AT27
25	33	76.7	640	5	Q9BLH9
26	33	76.7	927	16	Q9A579 caulobacter
27	33	76.7	4199	16	P74440 synecocyst
28	32	74.4	109	6	Q9N0W5
29	32	74.4	127	11	Q92S59
30	32	74.4	319	1	Q9V2T0
31	32	74.4	505	16	Q9KTE4
32	32	74.4	573	4	Q9NM44
33	32	74.4	583	4	Q9H587
34	32	74.4	596	2	Q917X7
35	32	74.4	846	4	Q9H9J6
36	32	74.4	858	4	Q9H7W7
37	32	74.4	1450	5	Q26627 strongyloce
38	32	74.4	1493	3	Q04002 saccharomyc
39	32	74.4	1865	2	Q9XCJ1
40	31	72.1	102	16	Q911U1
41	31	72.1	110	9	Q94MG5
42	31	72.1	110	9	Q94MC3
43	31	72.1	110	9	Q94MC2
44	31	72.1	110	9	Q94MC1
45	31	72.1	110	9	Q94MB9

ALIGNMENTS

RESULT 1
ID Q96SA9 PRELIMINARY: PRT: 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB6785.1; --
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BBA3E9C5B57FE16 CRC64;

Query Match 100.0%; Score 43; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTTSS 9
Db 69 TDFLTTSS 77
RESULT 2
ID Q9ERZ9 PRELIMINARY: PRT: 107 AA.

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AC 09ER29;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-TNF- $\alpha$  monoclonal antibody."
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF- $\alpha$  specific monoclonal antibody."
RL T1 4 Chun 1 Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (May-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF262753; ANG25804.1; -.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003599; I9.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003596; I9_V.
DR Pfam: PF00047; I9; 1.
DR SMART: SM00409; I9; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EFA6604A26C3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 11; Length 107;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
DB 72 TDFTLTSS 80

RESULT 3
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
OS "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
OC Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL: AF035037; AAD56273.1; -.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003596; I9_V.
DR Pfam: PF00047; I9; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41PCCA37 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 4; Length 108;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
DB 69 TDFTLTSS 77

RESULT 5
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;

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FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 4; Length 108;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
DB 69 TDFTLTSS 77

RESULT 4
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
OS "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
OC Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL: AF035044; AAD56280.1; -.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003596; I9_V.
DR Pfam: PF00047; I9; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41PCCA37 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 4; Length 108;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
DB 69 TDFTLTSS 77

RESULT 5
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;

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RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL: AF035033; AAD56269.1; -.
DR      HSSP: P01607; IREI.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; Igv; 1.
FT      NON_TER      1
FT      NON_TER      107
SQ      SEQUENCE      107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match
Best Local Similarity 90.7%; Score 39; DB 4; Length 107;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TDFTLTIS 8
DB      69 TDFTLTIS 76

RESULT  6
O9UL83  PRELIMINARY; PRT; 108 AA.
AC      O9UL83;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
      (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL: AF035031; AAD56267.1; -.
DR      HSSP: P80362; IWTL.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; Igv; 1.
FT      NON_TER      1
FT      NON_TER      108
SQ      SEQUENCE      108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match
Best Local Similarity 90.7%; Score 39; DB 4; Length 108;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 TDFTLTIS 9
DB      69 TDFTLTIS 77

RESULT  7
O9UL79  PRELIMINARY; PRT; 108 AA.
AC      O9UL79;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
      (FRAGMENT).

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OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL: AF035035; AAD56271.1; -.
DR      HSSP: P01607; IREI.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; Igv; 1.
FT      NON_TER      1
FT      NON_TER      108
SQ      SEQUENCE      108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match
Best Local Similarity 90.7%; Score 39; DB 4; Length 108;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TDFTLTIS 8
DB      69 TDFTLTIS 76

RESULT  8
O9UL86  PRELIMINARY; PRT; 109 AA.
AC      O9UL86;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
      (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL: AF035028; AAD56264.1; -.
DR      HSSP: P80362; IWTL.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; Igv; 1.
FT      NON_TER      1
FT      NON_TER      109
SQ      SEQUENCE      109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match
Best Local Similarity 90.7%; Score 39; DB 4; Length 109;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TDFTLTIS 8
DB      70 TDFTLTIS 77

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RESULT 9
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
   (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT 109
SQ SEQUENCE 109 AA; 11761 MW; FBIE43E7C7AFACCC CRC64;

Query Match
Best Local Similarity 90.7%; Score 39; DB 4; Length 109;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITIS 9
DB 69 TDFLTITIS 77

RESULT 10
Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
   (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
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Query Match
Best Local Similarity 90.7%; Score 39; DB 4; Length 109;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITIS 8
DB 70 TDFLTITIS 77
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RESULT 11
Q99XR2 PRELIMINARY; PRT; 557 AA.
AC Q99XR2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DE PUTATIVE FORMATE-TETRAHYDROFOLATE LIGASE (EC 6.3.4.3).
GN FHS.2 OR SPY2085.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lal H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006628; AAK34738.1; -.
DR InterPro; IPR000559; FTHFS.
DR Pfam; PF01268; FTHFS; 1.
DR PROSITE; PS00722; FTHFS_2; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 557 AA; 59053 MW; CB07C9FCE90B34E7 CRC64;
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```
Query Match
Best Local Similarity 86.0%; Score 37; DB 16; Length 557;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITIS 9
DB 505 TDFLTITIS 513

RESULT 12
Q9UL74 PRELIMINARY; PRT; 99 AA.
AC Q9UL74;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
   (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
   with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206032; AAF69330.1; -.
DR HSSP; P80362; 1WTL.
```

DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 FT NON_TER 1 99
 FT NON_TER 99 1
 SQ SEQUENCE 99 AA; 10939 MW; 3B5D0E784533324 CRC64;

Query Match 83.7%; Score 36; DB 11; Length 99;
 Best Local Similarity 77.8%; Pred. No. 4.2;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
 |||||
 Db 61 TDFTLTIST 69

RESULT 13
 Q96PF6 PRELIMINARY; PRT; 116 AA.
 ID Q96PF6;
 AC Q96PF6;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 GN SKN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21361171; PubMed-11468171;
 RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
 RT "The tropism of organ involvement in primary systemic amyloidosis:
 RT contributions of Ig V(L) germ line gene use and clonal plasma cell
 RT burden.";
 RL Blood 98:714-720(2001).
 DR EMBL; AF361758; AAK51465.1; -.
 FT NON_TER 1 116
 FT NON_TER 116 1
 SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 81.4%; Score 35; DB 4; Length 116;
 Best Local Similarity 77.8%; Pred. No. 8.1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
 |||||
 Db 69 TNETVTISS 77

RESULT 14
 Q929J3 PRELIMINARY; PRT; 1806 AA.
 ID Q929J3;
 AC Q929J3;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE PUTATIVE PEPTIDOGLYCAN BOUND PROTEIN (LPYTG MOTIF).
 GN LIN282.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Listeria.
 OC NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CLIP 11262 / SEROVAR 6A;
 RX PubMed-11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,

RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deloux P.,
 RA Doman E., Dominguez-Bernal G., Duchad E., Durant L., Dussurget O.,
 RA Entian K.-D., Esli H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkai G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordiel G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 DR EMBL; AL596171; CAC97510.1; -.
 DR Listlist: LIN02282; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1806 AA; 195670 MW; ABC808A65D84972F CRC64;

Query Match 81.4%; Score 35; DB 16; Length 1806;
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
 |||||
 Db 372 TDFTLTVSS 380

RESULT 15
 Q91GM1 PRELIMINARY; PRT; 284 AA.
 ID Q91GM1;
 AC Q91GM1;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE K1 GLYCOPROTEIN (FRAGMENT).
 GN K1.
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
 OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OC NCBI_TaxID=37296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-UGD7;
 RA Kakoola D.N., Sheldon J., Byabazaire N., Bowden R.J.,
 RA Katongole-Mbidde E., Schulz T.F., Davison A.J.;
 RT "Recombination in human herpesvirus 8 strains from Uganda and
 RT evolution of the K15 gene.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY042942; AAK72676.1; -.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 284 AA; 31804 MW; BA224B08EDDC38F CRC64;

Query Match 79.1%; Score 34; DB 12; Length 284;
 Best Local Similarity 77.8%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
 |||||
 Db 56 TDFTLTVSS 64

Search completed: July 15, 2002, 13:22:47
 Job time: 1483 sec

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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:57:58 ; Search time 228.39 seconds

(without alignments)
4.377 Million cell updates/sec

Title: US-09-712-819A-7

Perfect score: 43

Sequence: 1 TDFITLITSS 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.GeneSeq_032802:*

1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:*
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10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	32	17	AA87043
2	43	100.0	32	20	AA52745
3	43	100.0	32	22	AA598286
4	43	100.0	32	22	AA598288
5	43	100.0	32	22	AA597666
6	43	100.0	32	22	AA597668
7	43	100.0	74	19	AAW62805
8	43	100.0	76	20	AAW80981
9	43	100.0	82	19	AAW62807
10	43	100.0	84	17	AAW1491
11	43	100.0	84	17	AA99878

12	43	100.0	86	19	AAW62806
13	43	100.0	88	19	AAW59619
14	43	100.0	88	21	AAV56654
15	43	100.0	88	21	AAV56655
16	43	100.0	88	21	AAV56657
17	43	100.0	88	21	AAV56659
18	43	100.0	94	19	AAW62808
19	43	100.0	94	22	AAW67510
20	43	100.0	95	16	AAW72061
21	43	100.0	95	16	AAW72062
22	43	100.0	95	16	AAW72063
23	43	100.0	95	16	AAW72064
24	43	100.0	95	16	AAW72065
25	43	100.0	95	16	AAW72058
26	43	100.0	95	16	AAW72059
27	43	100.0	95	16	AAW72060
28	43	100.0	101	20	AAV54316
29	43	100.0	102	21	AAV56683
30	43	100.0	103	22	AAW54318
31	43	100.0	104	15	AAW54318
32	43	100.0	104	17	AAW01285
33	43	100.0	104	19	AAW62803
34	43	100.0	104	21	AAV95137
35	43	100.0	104	21	AAV98246
36	43	100.0	105	15	AAW54310
37	43	100.0	105	17	AAW01268
38	43	100.0	105	17	AAW98495
39	43	100.0	105	17	AAW98497
40	43	100.0	105	17	AAW88717
41	43	100.0	105	19	AAW52243
42	43	100.0	105	19	AAW52231
43	43	100.0	105	19	AAW52237
44	43	100.0	105	19	AAW52239
45	43	100.0	105	19	AAW52241

ALIGNMENTS

RESULT 1

ID AA87043 standard; Peptide; 32 AA.

AC AA87043;

DE 25-JUN-1996 (first entry)

XX Human group I light chain framework 3.

DE Humanised antibody; interleukin-5; IL-5; recombinant antibody;

XX antibody engineering; monoclonal antibody; MAb; 39D10; CDR;

KW complementarity determining region; light chain; framework;

KW eosinophilia; allergy; asthma.

XX Homo sapiens.

OS W09535375-A1.

XX 28-DEC-1995.

PD 16-JUN-1995; 95WO-GB01411.

XX 17-JUN-1994; 94GB-0012230.

PR (CULT) CELLTECH THERAPEUTICS LTD.

PA Athwal DS, Bodmer MW, Emlage JS;

XX WPI; 1996-058412/06.

DR Anti-human IL-5 recombinant antibody - useful for preventing or

PT reducing eosinophilia and for treating certain allergic diseases,

PT esp. asthma

Example 3; Fig 3; 69pp; English.

Framework regions (AAR87041-44) of human group I (gpl) gene line antibody light chain showed homology to corresponding regions (AAR87045-48, respectively) of the rat anti-human interleukin-5 monoclonal antibody 39D10 light chain (see AAR87040). This homology was utilised in the prodn. of a humanised 39D10 VL (AAR87057) in which rat 39D10 VL complementarity determining regions were grafted into the human gpl framework.

SQ Sequence 32 AA;

```

Query Match      100.0%; Score 43; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TDFILTLISS 9
    |||||
Ob 13 tdfiltiliss 21

```

RESULT 2

ID AAY52745 standard; Peptide; 32 AA.

AC AAY52745

DT 26-JAN-2000 (first entry)

DE Humanised ATR-5 L chain V region FR3 for "a"

Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody; ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC; disseminated intravascular coagulation; immunogenicity; chimeric.

05 Synthetic.

OS Homo sapiens.

PN W09951743-A1.

PD 14-OCT-1999.

PF 02-APR-1999; 99WO-JP01768.

PR 03-APR-1998; 98JP-0091850.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Sato K, Adachi H, Yabuta N;

DR WPI: 1999-620204/53.

PT Humanised antibody recognizing human tissue factor, used for treatment of disseminated intravascular coagulation -

PS Claim 17; Page 270; 291pp; Japanese.

CC The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (hrTF) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab Light (L)
CC chains containing the variable region of the L chain of a mouse
CC monoclonal Ab recognising human tissue factor (hrTF) and the constant
CC region of the L chain of a human Ab, the variable region being one of six
CC specified sequences (which are the L chain variable regions from mouse
CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
CC the treatment and prevention of thrombotic disease, especially of
CC disseminated intravascular coagulation (DIC). The humanised antibody has
CC the high hrTF binding activity of the mouse monoclonal antibody but

CC greatly reduced immunogenicity. AAZ33001 to AAZ33091 and Y527007 to
CC AAY5767 represent sequences used in the exemplification of the present
CC invention.

SQ Sequence 32 AA;

```

Query Match          100.0%; Score 43; DB 20; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TDPFTLIS 9
    ||| ||| |||
Db 13 tdfcltiss 21

```

RESULT 3

ID AAB98286 standard; Peptide; 32 AA.

AC AAB98286;
yy

DT 20-AUG-2001 (first entry)

DE Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:92.

KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
 KW immunoglobulin; complementarity determining region; CDR; cancer;
 KW cytostatic; anticancer; colon cancer; stomach cancer.

OS Homo sapiens.

PN W0200130393-A2

PD 03-MAY-2001.

PF 20-OCT-2000; 2000WO-US29289.

PR 22-OCT-1999; 99US-0425638 -

[illegible]

```
PA (SLOK ) SLOAN KETTERING INST CANCER RES
PA (SCRI ) SCRIPPS RES INST.
```

PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ

DR WPI; 2001-328613/34

AA Treating cancers, particularly of stomach and colon, that express A33
PT antigen by administering conjugate of anticancer agent with specific
PT immunoglobulin product -

PS Claim 16; Page 40; 85pp; English.

The present invention describes a method for treating cancers that express the A33 antigen. The method comprises administering an anticancer agent (i) conjugated to an immunoglobulin product (ii) that binds specifically to A33 and contains one or more of 13 specified complementarily determining regions (CDRs), given in AAB88262 to AAB88274. (i) has cytostatic activity. The method can be used for treating colon and stomach cancers. (ii), or the nucleic acid encoding it, can be used directly, in unconjugated form, for immunotherapy of cancer, and, when labeled, for detection or diagnosis of diseases associated with A33 expression. AA122218 to AA122254 and AA198330 to AA198331 represent sequences used in the exemplification of the present invention.

Sequence	32 AA
SQ	

Query Match	100.0%;	Score 43;	DB 22;	Length 32;
Best Local Similarity	100.0%;	Pred. No. 0.13;		

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
 |||||||
 DB 13 tdfLtlss 21

RESULT 4
 AAB98288
 ID AAB98288 standard; Peptide; 32 AA.
 XX
 AC AAB98288;
 XX
 DE 20-AUG-2001 (first entry)
 XX
 DE Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:94.
 XX
 KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
 KW immunoglobulin; complementarity determining region; CDR; cancer;
 KW cytostatic; anticancer; colon cancer; stomach cancer.
 XX
 OS Homo sapiens.
 XX
 PA WO200130393-A2.
 PN
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-US29289.
 XX
 PR 22-OCT-1999; 99US-0425638.
 PR 04-APR-2000; 2000US-0543004.
 XX
 PA (LUDWIG-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C, Rittler G, Welt S, Old LJ;
 XX
 DR WPI; 2001-328613/34.
 XX
 PT Treating cancers, particularly of stomach and colon, that express A33
 PT antigen by administering conjugate of anticancer agent with specific
 PT immunoglobulin product -
 XX
 PS Claim 16; Page 40; 85pp; English.
 XX
 CC The present invention describes a method for treating cancers that
 CC express the A33 antigen. The method comprises administering an
 CC anticancer agent (I) conjugated to an immunoglobulin product (II) that
 CC binds specifically to A33 and contains one or more of 13 specified
 CC complementarity determining regions (CDRs), given in AAB98282 to
 CC AAB98274. (I) has cytostatic activity. The method can be used for
 CC treating colon and stomach cancers. (II), or the nucleic acid encoding
 CC it, can be used directly, in unconjugated form, for immunotherapy of
 CC cancer, and, when labeled, for detection or diagnosis of diseases
 CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
 CC AAB98321 represent sequences used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 43; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
 |||||||
 DB 13 tdfLtlss 21

RESULT 5
 AAB97666

ID AAB97666 standard; Peptide; 32 AA.
 XX
 AC AAB97666;
 XX
 DE 08-AUG-2001 (first entry)
 XX
 DE A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:92.
 XX
 KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
 KW Immunoreact; anti A33 antigen antibody; immunoglobulin.
 XX
 OS Homo sapiens.
 XX
 PA WO200131065-A1.
 PN
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-US29026.
 XX
 PR 22-OCT-1999; 99US-0425638.
 PR 04-APR-2000; 2000US-0543004.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 2001-328657/34.
 XX
 PT Preparing humanized rabbit antibodies that specifically immunoreact
 PT with a particular antigen using display technology for expressing
 PT libraries of antibody domains and fine tuning variable domain regions -
 XX
 PS Example 9; Page 39; 62pp; English.
 XX
 CC The present invention describes a method for preparing a humanised rabbit
 CC antibody that specifically immunoreacts with a particular antigen. The
 CC method comprises expressing a library of antibodies comprising one or
 CC more complementarity determining region (CDR) from the variable domain
 CC sequences that specifically immunoreact with the antigen grafted into
 CC framework regions from humans, and selecting the antibodies that react
 CC with the antigen. The method is useful for humanising non-human
 CC mammalian antibodies, which can be used for the treatment of a variety
 CC of diseases. The present sequence represents an A33 antigen binding
 CC immunoglobulin product VLFR3 peptide which is given in an example from
 CC the present invention.
 XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 43; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
 |||||||
 DB 13 tdfLtlss 21

RESULT 6
 AAB97668
 ID AAB97668 standard; Peptide; 32 AA.
 XX
 AC AAB97668;
 XX
 DE 08-AUG-2001 (first entry)
 XX
 DE A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:94.
 XX
 KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
 KW Immunoreact; anti A33 antigen antibody; immunoglobulin.
 XX
 OS Homo sapiens.
 XX

PT - useful to treat solid tumours whilst inducing reduced immunogenic
or allergic effects compared to mouse or mouse-derived antibodies
XX
PS Example 3; Page 105; 143pp; English.
XX
CC The variable kappa light region 012 encoded amino acid was used in the
CC production of anti-epidermal growth factor receptor (EGF-r)-antibodies.
CC The antibodies can be administered therapeutically to patients (human or
CC veterinary) to treat solid tumours. EGF-r is overexpressed on many human
CC solid tumour types, and the fully human antibodies (i.e. comprising and
CC inhibit both epidermal growth factor (EGF) and transforming growth factor
CC alpha (TGF-alpha) binding to EGF-r (known to prevent tumour cell growth
CC proliferation and tumour growth). They can prevent tumour cell growth
CC and, in combination with an antineoplastic agent, may eradicate
CC established tumours. The fully human antibodies can minimise the
CC immunogenic and allergic responses intrinsic to previous mouse/rat or
CC mouse/rat-derived antibodies.
XX
SQ Sequence 76 AA;

Query Match 100.0%; Score 43; DB 20; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTIS 9
| | | | | | | |
DB 50 tdfTLtIs 58

RESULT 9
AAW62807
ID AAW62807 standard; Peptide; 82 AA.
XX
AC AAW62807;
XX
DT 23-SEP-1998 (first entry)
XX
DE Amino acid sequence of a human antibody fragment.
XX
KW Human; Immunoglobulin; Ig; transgenic; non-human mammal;
KW inactivated endogenous Ig locus; B-cell development;
KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW production; antibody.
XX
OS Homo sapiens.
XX
PN MO9824893-A2.
XX
PD 11-JUN-1998.
XX
PF 03-DEC-1997; 97WO-US23091.
XX
PR 03-DEC-1996; 96US-0759620.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Green L; Jakobovits A; Klapholz S; Kucherlapati R;
PI Mendez M;
XX
DR WPI; 1998-33314/29.
XX
PT New transgenic non-human mammals - having an inactivated
PT immunoglobulin locus and a near complete human immunoglobulin locus,
PT used for production of human antibodies
XX
PS Disclosure: Page 78; 128pp; English.
XX
CC AAW62793-822 represent fragments of human antibodies produced by
CC transgenic xenomice, created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)

CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in
CC germine configuration, the human heavy chain Ig locus comprising a human
CC micro constant region and regulatory and switch sequences, human J-H
CC genes, human D-H genes, and human V-H genes and an inserted human kappa
CC light chain Ig locus in germine configuration, the human kappa light
CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC and V-kappa genes, where the number of V-H and V-kappa genes inserted
CC are selected to restore normal B-cell development in the mammal. The
CC transgenic animals have a near complete human Ig locus, including both a
CC human heavy chain locus and a human kappa light chain locus. They can
CC be used for the production of human antibodies when exposed to
CC particular antigens e.g. when exposed to human IL-8, EGF or TNF- alpha
CC the mice will produce antibodies to IL-8, EGF or TNF- alpha
XX
SQ Sequence 82 AA;

Query Match 100.0%; Score 43; DB 19; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTIS 9
| | | | | | | |
DB 56 tdfTLtIs 64

RESULT 10
AAW14491
ID AAW14491 standard; Protein; 84 AA.
XX
AC AAW14491;
XX
DT 28-JAN-1997 (first entry)
XX
DE Monoclonal antibody D VK.
XX
KW heavy; light chain; monoclonal antibody; antigen 3; marker; melanoma;
KW permanent human tumour cell line; tumour-associated antigen; epitope;
KW gastrointestinal tumour; pancreatic carcinoma; diagnostic; therapeutic;
KW antigen 11; Vibrio cholera; neuraminidase-resistant; ganglioside GD2.
XX
OS Synthetic.
XX
PN EP727436-A1.
XX
PD 21-AUG-1996.
XX
PF 21-MAR-1990; 90EP-0105322.
XX
PR 24-MAR-1989; 89DE-3909799.
XX
PA (BEHM) BEHRINGWERKE AG.
XX
PI Auerbach B, Bosslet K, Sedlacek H, Seemann G;
PI WPI; 1996-372836/38.
XX
DR N-PSDB; AAT63508.
XX
PT Monoclonal antibody to tumour-associated antigen - useful as
PT gastrointestinal tumour marker
XX
PS Disclosure: Page 14; 19pp; German.
XX
CC AAW14490-91 are the heavy and light chains (respectively) of monoclonal
CC antibody (MAb) D. MAb D recognises Vibrio cholera
CC neuraminidase-resistant epitope of ganglioside GD2, from a human melanoma
CC cell line. Mabs A, B and C (see AAW14484-89) are mentioned in the
CC specification, but are not part of the claims. Mabs A and B recognise
CC antigens 3 and 11 resp., of a permanent human tumour cell line. MAb C
CC also recognises an epitope of a tumour-associated antigen. These antigens
CC occur at high concns. in the serum of patients with gastrointestinal

CC tumours, e.g. pancreatic carcinoma, and are thus useful as tumour markers
CC for diagnostic or therapeutic purposes.

XX Sequence 84 AA;

Query Match 100.0%; Score 43; DB 17; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTSS 9
Db 47 tdfcltiss 55

RESULT 11
AAR9878
ID AAR9878 standard; Protein: 84 AA.

XX AAR9878;

XX 28-JAN-1997 (first entry)

XX Monoclonal antibody D VK.

XX Monoclonal antibody; Mab; epitope: tumour-associated antigen;

XX marker; antigen.

XX Synthetic.

XX EP727435-A1.

XX 21-AUG-1996.

XX 21-MAR-1990; 90EP-0105322.

XX 24-MAR-1989; 89DE-3909799.

XX (BEHM) BEHRINGWERKE AG.

XX Auerbach B, Boslet K, Sedlacek H, Seemann G;

XX WPI: 1996-372835/38.

XX N-PSDB; AAT36666.

XX Monoclonal antibody to tumour-associated antigen - useful as

XX gastrointestinal tumour marker

XX Disclosure: Page 14; 19pp; German.

XX Mab C (AAT36659-736660) is a monoclonal antibody that recognises an

XX epitope of a tumour-associated antigen occurring at high concn. in

XX the serum of patients with gastrointestinal tumours, e.g. pancreatic

XX carcinoma, and is thus useful as a tumour marker for diagnostic or

XX therapeutic purposes.

XX Mabs A, B and D are mentioned in the specification, but are not

XX part of the claims.

XX Mab A (AAT36661-736662) recognises antigen 3 of permanent human

XX tumour cell line.

XX Mab B (AAT36663-736664) recognises antigen 11 of permanent human

XX tumour cell line.

XX Mab D (AAT36665-736666) recognises a Vibrio cholera neuraminidase-

XX resistant epitope of ganglioside GD2, from a human melanoma cell

XX line.

XX Sequence 84 AA;

Qy 1 TDFTLTSS 9

Query Match 100.0%; Score 43; DB 17; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 47 tdfcltiss 55

RESULT 12

AAW62806
ID AAW62806 standard; Peptide: 86 AA.

XX AAW62806;

XX 23-SEP-1998 (first entry)

XX Amino acid sequence of a human antibody fragment.

XX Human; immunoglobulin; Ig; transgenic; non-human mammal;

XX inactivated endogenous Ig locus; B-cell development;

XX human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;

XX kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;

XX production; antibody.

XX Homo sapiens.

XX W09824893-A2.

XX 11-JUN-1998.

XX 03-DEC-1997; 97WO-US23091.

XX 03-DEC-1996; 96US-0759620.

XX (ABGE-) ABGENIX INC.

XX Green L, Jakobovits A, Klapholz S, Kucheriapali R;

XX Mendez M;

XX WPI: 1998-333314/29.

XX New transgenic non-human mammals - having an inactivated

XX immunoglobulin locus and a near complete human immunoglobulin locus,

XX used for production of human antibodies

XX Disclosure: Page 78; 128pp; English.

XX AAW62793-822 represent fragments of human antibodies produced by

XX transgenic Xenomice, created using the method of the invention. The

XX specification describes a transgenic non-human mammal which has genome

XX modifications that comprise an inactivated endogenous immunoglobulin (Ig)

XX locus, so that the mammal does not display normal B-cell development. The

XX modified genome also has an inserted human heavy chain Ig locus in

XX germ-line configuration, the human heavy chain Ig locus comprising a human

XX micro constant region and regulatory and switch sequences, human J-H

XX genes, human D-H genes, and human V-H genes and an inserted human kappa

XX light chain Ig locus in germ-line configuration, the human kappa light

XX chain Ig locus comprising a human kappa constant region, J-kappa genes,

XX and V-kappa genes, where the number of V-H and V-kappa genes inserted

XX are selected to restore normal B-cell development in the mammal. The

XX transgenic animals have a near complete human Ig locus, including both a

XX human heavy chain locus and a human kappa light chain locus. They can

XX be used for the production of human antibodies when exposed to

XX particular antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha

XX the mice will produce antibodies to IL-8, EGFR or TNF- alpha

XX respectively.

XX Sequence 86 AA;

Qy 1 TDFTLTSS 9

Query Match 100.0%; Score 43; DB 19; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 48 tdfcltiss 56

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RESULT 13
ID AAM59619 standard; Protein; 88 AA.
XX
AC AAM59619;
XX
DT 12-OCT-1998 (first entry)
XX
DE Anti-RSV F protein Hu19 light chain GL Dpk9.
XX
KM Monoclonal antibody; human; Hu19; engineered antibody; RSV;
KW respiratory syncytial virus; fusion protein; infection;
XX complementarity determining region; CDR; therapy; diagnosis.
OS Homo sapiens.
XX
FH Key
FT Region 24..34 Location/Qualifiers
FT 50..57 /label= CDR1
FT /label= CDR2
XX
PN WO9819704-A1.
XX
PD 14-MAY-1998.
XX
PF 23-OCT-1997; 97WO-US19203.
XX
PR 01-NOV-1996; 96US-0030149.
XX
PA (SMK ) SMITHKLINE BEECHAM CORP.
XX
PI Deen KC, Dillon SB, Porter TG, Sweet RM;
XX
DR WPI; 1998-286600/25.
XX
PT Monoclonal antibodies reactive with Respiratory Syncytial Virus -
XX useful for detection, prevention and treatment of RSV infections
XX
PS Disclosure; Fig 3; 109pp; English.
XX
SQ
CC This is the heavy chain amino acid sequence of germline (GL)
CC DPK9 antibody. The invention relates to the construction and use
CC of human MAb's specific for the fusion (F) protein of respiratory
CC syncytial virus (RSV) to passively treat, prevent or detect RSV
CC infection. Hu19A, Hu19B, Hu19C and Hu19D MAb's are claimed. These
CC are reshaped human antibodies comprising a heavy chain selected
CC from 19A, 19B, 19C or 19D (see AAM59615-18), which are based on the
CC GL DPK9 sequence, and a light chain selected from 19A, 19B, 19C or
CC 19D (see AAM59620-21). Such engineered antibodies are neutralising;
CC they inhibit virus growth in vitro and in vivo in animal models of
CC RSV infection. Nucleic acids encoding the human MAb's recombinant
CC plasmids (see AAV41427-33) and host cells (e.g. COS, CHO, myeloma)
CC are provided.
XX
SQ Sequence 88 AA:

Query Match 100.0%; Score 43; DB 19; Length 88;
Best Local Similarity 100.0%; Pred. NO. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
DB 69 tdfTLtIs 77

RESULT 14
AAV56654
ID AAV56654 standard; protein; 88 AA.
XX

```

```

AC AAY56654;
XX
DT 15-FEB-2000 (first entry)
XX
DE Partial peptide fragment of chimpanzee V kappa cDNA clone 46-5.
XX
KM Complementarity determining region; antibody; primate; immunogenicity;
KW Old World ape; Old World monkey; antigen-binding affinity.
XX
OS Pan troglodytes.
XX
PN WO995369-A1.
XX
PD 04-NOV-1999.
XX
PF 28-APR-1999; 99WO-US09131.
XX
PR 28-APR-1998; 98US-0083367.
XX
PA (SMK ) SMITHKLINE BEECHAM CORP.
XX
PI Taylor AH;
XX
DR WPI; 2000-023265/02.
XX
DR N-PSDB; AAZ39322.
XX
PT Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
PT humans -
XX
PS Claim 22; Page 70-71; 123pp; English.
XX
SQ
CC The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarity determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.
XX
SQ Sequence 88 AA:

Query Match 100.0%; Score 43; DB 21; Length 88;
Best Local Similarity 100.0%; Pred. NO. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
DB 69 tdfTLtIs 77

RESULT 15
AAV56655
ID AAV56655 standard; protein; 88 AA.
XX
AC AAY56655;
XX
DT 15-FEB-2000 (first entry)
XX
DE Partial peptide fragment of chimpanzee V kappa cDNA clone 46-6.
XX
KM Complementarity determining region; antibody; primate; immunogenicity;
KW Old World ape; Old World monkey; antigen-binding affinity.
XX
OS Pan troglodytes.
XX
PN WO995369-A1.
XX
PD 04-NOV-1999.
XX

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PF 28-APR-1999; 99WO-US09131.
XX
PR 28-APR-1998; 98US-0083367.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Taylor AH;
XX
DR WPI: 2000-023265/02.
DR N-PSDB: AA239323.
XX
PT Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
PT humans -
XX
PS Claim 22; Page 71; 123pp; English.
XX
CC The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarity determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.
XX
SQ Sequence 88 AA;

Query Match 100.0%; Score 43; DB 21; Length 88;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTIS 9
|||
Db 69 tdfiltis 77

Search completed: July 15, 2002, 12:57:58
Job time: 414 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 12:59:19 ; Search time 75.67 Seconds
(without alignments)
2.905 Million cell updates/sec

Title: US-09-712-819A-7
Perfect score: 43
Sequence: 1 TDFLTITSS 9

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/prodata/2/1aa/5H_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	25 5	PCT-US91-02942-42	Sequence 42, Appl
2	43	100.0	32 2	US-08-470-139-13	Sequence 13, Appl
3	43	100.0	32 4	US-08-569-147-40	Sequence 40, Appl
4	43	100.0	32 4	US-09-347-061-13	Sequence 13, Appl
5	43	100.0	32 4	US-09-425-638A-92	Sequence 92, Appl
6	43	100.0	32 4	US-09-425-638A-94	Sequence 94, Appl
7	43	100.0	32 4	US-09-543-004-92	Sequence 92, Appl
8	43	100.0	32 4	US-09-543-004-94	Sequence 94, Appl
9	43	100.0	50 5	PCT-US91-02942-9	Sequence 9, Appl
10	43	100.0	64 2	US-08-765-179B-10	Sequence 10, Appl
11	43	100.0	64 2	US-08-765-179B-14	Sequence 14, Appl
12	43	100.0	70 3	US-08-554-840-9	Sequence 9, Appl
13	43	100.0	76 4	US-08-851-362D-21	Sequence 21, Appl
14	43	100.0	80 3	US-08-554-840-12	Sequence 12, Appl
15	43	100.0	80 3	US-08-554-840-13	Sequence 13, Appl
16	43	100.0	80 3	US-08-554-840-15	Sequence 15, Appl
17	43	100.0	80 3	US-08-554-840-15	Sequence 15, Appl
18	43	100.0	93 3	US-08-783-853A-35	Sequence 35, Appl
19	43	100.0	96 3	US-08-466-368-6	Sequence 6, Appl
20	43	100.0	103 4	US-09-240-274-42	Sequence 42, Appl
21	43	100.0	104 1	US-08-276-852-106	Sequence 106, App
22	43	100.0	104 1	US-08-899-575-106	Sequence 106, App
23	43	100.0	104 1	US-08-899-575-106	Sequence 106, App
24	43	100.0	104 1	PCT-US95-08743-106	Sequence 106, App
25	43	100.0	105 1	US-08-276-852-89	Sequence 89, Appl
26	43	100.0	105 1	US-08-899-575-89	Sequence 89, Appl
27	43	100.0	105 5	US-08-899-575-89	Sequence 89, Appl

28	43	100.0	106 1	US-08-276-852-83	Sequence 83, Appl
29	43	100.0	106 1	US-08-276-852-85	Sequence 85, Appl
30	43	100.0	106 1	US-08-899-575-83	Sequence 83, Appl
31	43	100.0	106 1	US-08-899-575-85	Sequence 85, Appl
32	43	100.0	106 1	US-08-899-575-83	Sequence 83, Appl
33	43	100.0	106 1	US-08-899-575-85	Sequence 85, Appl
34	43	100.0	106 3	US-08-397-411-8	Sequence 8, Appl
35	43	100.0	106 4	US-09-240-274-159	Sequence 159, App
36	43	100.0	106 4	US-09-240-274-165	Sequence 165, App
37	43	100.0	106 5	PCT-US95-08743-83	Sequence 83, Appl
38	43	100.0	106 5	PCT-US95-08743-85	Sequence 85, Appl
39	43	100.0	107 1	US-07-634-278-103	Sequence 103, App
40	43	100.0	107 1	US-08-477-728-103	Sequence 103, App
41	43	100.0	107 1	US-08-276-852-82	Sequence 82, Appl
42	43	100.0	107 1	US-08-276-852-84	Sequence 84, Appl
43	43	100.0	107 1	US-08-276-852-104	Sequence 104, App
44	43	100.0	107 1	US-08-276-852-105	Sequence 105, App
45	43	100.0	107 1	US-08-300-386A-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
PCT-US91-02942-42
Sequence 42, Application PC/FUS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADAIR, JOHN R
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox,
STREET: 1225 Connecticut Ave. NW Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 19910429
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0586600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02942-42

Query Match 100.0%; Score 43; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.058; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0

QY 1 TDFLTITSS 9
|||||

Db 6 TDFLTITSS 14

RESULT 2
US-08-470-139-13
Sequence 13, Application US/08470139
Patent No. 5996586
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,139
FILING DATE: 06 JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOREEN YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0044
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-470-139-13

Query Match 100.0%; Score 43; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
|||||
Db 13 TDFLTITSS 21

RESULT 3
US-08-569-147-40
Sequence 40, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSER: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOREEN YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-569-147-40

Query Match 100.0%; Score 43; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
|||||
Db 13 TDFLTITSS 21

RESULT 4
US-09-347-061-13
Sequence 13, Application US/09347061
Patent No. 6316227
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark
APPLICANT: Athwal, Diljeet Singh
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0071
CURRENT APPLICATION NUMBER: US/09/347,061
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Consensus
US-09-347-061-13

Query Match 100.0%; Score 43; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
|||||
Db 13 TDFLTITSS 21

RESULT 5
US-09-425-638A-92
Sequence 92, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt an
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THE
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 92
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-92

Query Match 100.0%; Score 43; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
Db 13 TDFTLTSS 21

RESULT 6

US-09-425-638A-94
; Sequence 94, Application US/09425638A
; Patent No. 6342587

; GENERAL INFORMATION:

; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old

; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF

; FILE REFERENCE: LUD 5630

; CURRENT APPLICATION NUMBER: US/09/425,638A

; CURRENT FILING DATE: 1999-10-22

; NUMBER OF SEQ ID NOS: 129

; SEQ ID NO 94

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

US-09-425-638A-94

Query Match 100.0%; Score 43; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
Db 13 TDFTLTSS 21

RESULT 7

US-09-543-004-92
; Sequence 92, Application US/09543004
; Patent No. 6346249

; GENERAL INFORMATION:

; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old

; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF

; FILE REFERENCE: LUD 5630.1

; CURRENT APPLICATION NUMBER: US/09/543,004

; CURRENT FILING DATE: 2000-04-04

; PRIOR APPLICATION NUMBER: 09/425,638

; PRIOR FILING DATE: 1999-10-22

; NUMBER OF SEQ ID NOS: 129

; SEQ ID NO 92

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

US-09-543-004-92

Query Match 100.0%; Score 43; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
Db 13 TDFTLTSS 21

RESULT 8

US-09-543-004-94
; Sequence 94, Application US/09543004

; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old

; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF

; FILE REFERENCE: LUD 5630.1

; CURRENT APPLICATION NUMBER: US/09/543,004

; CURRENT FILING DATE: 2000-04-04

; PRIOR APPLICATION NUMBER: 09/425,638

; PRIOR FILING DATE: 1999-10-22

; NUMBER OF SEQ ID NOS: 129

; SEQ ID NO 94

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

US-09-543-004-94

Query Match 100.0%; Score 43; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
Db 13 TDFTLTSS 21

RESULT 9

PCT-US91-02942-9
; Sequence 9, Application PC/TUS9102942
; GENERAL INFORMATION:

; APPLICANT: ROTHLEIN, ROBERT

; APPLICANT: ADAIR, JOHN R

; APPLICANT: ATHWAL, DILJEET S

; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY

; NUMBER OF SEQUENCES: 102

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1225 Connecticut Ave. NW Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/02942

FILING DATE: 19910429

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9009549.8

FILING DATE: 27-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: FOX, SAM L

REGISTRATION NUMBER: 30,353

REFERENCE/DOCKET NUMBER: 1011,0586600

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 466-0800

TELEFAX: (202) 833-8716

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US91-02942-9

Query Match 100.0%; Score 43; DB 5; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TDFLTITSS 9
Db 24 TDFLTITSS 32

RESULT 10
US-08-765-179B-10
; Sequence 10, Application US/08765179B
; Patent No. 5854027
; GENERAL INFORMATION:
; APPLICANT: STEINBACHER, Boris
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
; TITLE OF INVENTION: OF ANTIBODIES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,179B
; FILING DATE: 14-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02626
; FILING DATE: 06-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 25 115.7
; FILING DATE: 15-JUL-1994
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-179B-10

Query Match 100.0%; Score 43; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
Db 38 TDFLTITSS 46

RESULT 11
US-08-765-179B-14
; Sequence 14, Application US/08765179B
; Patent No. 5854027
; GENERAL INFORMATION:
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
; TITLE OF INVENTION: OF ANTIBODIES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,179B
FILING DATE: 14-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 25 115.7
FILING DATE: 15-JUL-1994
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-179B-14

Query Match 100.0%; Score 43; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
Db 38 TDFLTITSS 46

RESULT 12
US-08-554-840-9
; Sequence 9, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-9

Query Match 100.0%; Score 43; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
|||||
DB 51 TDFTLTSS 59

RESULT 13
US-08-851-362D-21
Sequence 21, Application US/08851362D
Patent No. 6235883
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 76
TYPE: PRT
ORGANISM: human
US-08-851-362D-21

Query Match 100.0%; Score 43; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
|||||
DB 50 TDFTLTSS 58

RESULT 14
US-08-554-840-12
Sequence 12, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabli
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-12

Query Match 100.0%; Score 43; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
|||||
DB 51 TDFTLTSS 59

RESULT 15
US-08-554-840-13
Sequence 13, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabli
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-554-840-13

Query Match 100.0%; Score 43; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TDFTLTSS 9
|||||||
Db 51 TDFTLTSS 59

Search completed: July 15, 2002, 12:59:19
Job time: 390 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:01:02 ; Search time 95.45 seconds

(without alignments)
11.074 Million cell updates/sec

Title: US-09-712-819A-8

Perfect score: 58

Sequence: 1 YGRRKRRORRKK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_71:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	89.7	86	1	TN1JND
2	49	84.5	71	2	T09384
3	49	84.5	72	1	TN1JH4
4	49	84.5	86	1	TN1J2R
5	49	84.5	86	2	A25700
6	49	84.5	86	2	S54381
7	49	84.5	86	2	S33982
8	49	84.5	86	2	JC5591
9	49	84.5	87	2	T01665
10	49	84.5	95	1	TN1J12
11	49	84.5	101	1	E44001
12	49	84.5	101	2	T09446
13	43	74.1	250	2	D38095
14	43	74.1	268	2	C38095
15	43	74.1	269	2	A38095
16	43	74.1	269	2	B38095
17	43	74.1	272	2	A38900
18	43	74.1	279	2	JH0402
19	43	74.1	303	2	JH0401
20	43	74.1	366	2	S61796
21	43	74.1	525	2	T46824
22	43	74.1	1022	2	S49127
23	42	72.4	128	2	H70457
24	42	72.4	431	2	S48908
25	42	72.4	552	2	JC4030
26	42	72.4	587	2	E96702
27	41	70.7	371	2	B38625
28	41	70.7	397	2	A39565
29	41	70.7	399	2	A39625

30	41	70.7	793	2	JC5539	Smoothed protein
31	40	69.0	509	2	A96563	probable protein k
32	39	67.2	148	2	S04807	hypothetical prote
33	39	67.2	153	2	T10115	replication-associ
34	39	67.2	333	2	JC7713	ankyrin-repeat pro
35	39	67.2	411	1	00CVP2	p1 polypeptide
36	39	67.2	643	2	S46723	arginine-CRMA 11g
37	39	67.2	743	2	E84767	hypothetical prote
38	39	67.2	747	1	A57107	kinesin-related pr
39	39	67.2	826	2	D86458	hypothetical prote
40	38	65.3	144	2	S46716	hypothetical prote
41	38	65.5	261	2	T09075	hypothetical prote
42	38	65.5	478	1	DPHDM2	methionyl aminopep
43	38	65.5	480	2	A46702	methionyl aminopep
44	38	65.5	517	2	T49173	hypothetical prote
45	38	65.5	683	2	T00872	probable protein k

ALIGNMENTS

RESULT 1
TN1JND
Trans-activating transcription regulator - human immunodeficiency virus type 1 (isola
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:date: 30-Sep-1991 #sequence-revision 30-Sep-1991 #text-change 16-Jul-1999
C:Accession: J00071
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,
Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human imm
A:Reference number: J00065; MUID:90034200
A:Accession: J00071
A:Molecule type: DNA
A:Residues: 1-86 <SP>
A:Cross-references: GB:M27323; NID:9328154; PIDN:AAA44866.1; PID:9328155
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; immunodeficiency; transcription

Query Match 89.7%; Score 52; DB 1; Length 86;
Best Local Similarity 81.8%; Pred. No. 0.15;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRORRKK 11
|||||||:
Db 47 YGRRKRRORRKK 57

RESULT 2
T09384
Trans-activating transcription regulator - human immunodeficiency virus type 1 (isola
C:Species: human immunodeficiency virus type 1, HIV-1
C:date: 11-Jun-1999 #sequence-revision 11-Jun-1999 #text-change 21-Jul-2000
C:Accession: T09384
R:Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.;
J. Virol. 69, 4228-4236, 1995
A:Title: Defective accessory genes in a human immunodeficiency virus type 1-infected
A:Reference number: Z16654; MUID:95287475
A:Accession: T09384
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-71 <MC>
A:Cross-references: EMBL:U24451; NID:9829440; PIDN:AAA79576.1; PID:9829444
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: transcription

Query Match 84.5%; Score 49; DB 2; Length 71;

Best Local Similarity 72.7%; Pred. No. 0.39;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRRKRRQKK 11
|||||
Db 47 YGRRKRRQRR 57

RESULT 3
TNLRH4
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 02-Jul-1998
C:Accession: B25523
R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,
Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
A:Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human
A:Reference number: A94136; MUID:87041461
A:Accession: B25523
A:Molecule type: DNA
A:Residues: 1-72 <DES>
A:Cross-references: GB:M13137; NID:g326460
A:Note: the Genbank entry ADR63AA PID:g209908 differs from the published sequence in trn
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: transcription regulation

Query Match 84.5%; Score 49; DB 1; Length 72;
Best Local Similarity 72.7%; Pred. No. 0.39;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRRKRRQKK 11
|||||
Db 47 YGRRKRRQRR 57

RESULT 4
TNLRH4
trans-activating transcription regulator - human immunodeficiency virus 2r-6
C:Species: human immunodeficiency virus 2r-6
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C:Accession: G26192
R:Srinivasan, A.; Anand, R.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti
A:Reference number: A26192; MUID:87248097
A:Accession: G26192
A:Molecule type: DNA
A:Residues: 1-86 <SRH>
A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA5377.1; PID:g329400
C:Genetics:
A:Gene: tat
A:Introns: 72/3
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 84.5%; Score 49; DB 1; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.45;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRRKRRQKK 11
|||||
Db 47 YGRRKRRQRR 57

RESULT 5
A25700
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 02-Jul-1998

C:Accession: A25700
R:Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, W.
Science 229, 74-77, 1985
A:Reference number: A25700; MUID:85244627
A:Accession: A25700
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-86 <SOD>
C:Superfamily: AIDS trans-activating transcription regulator

Query Match 84.5%; Score 49; DB 2; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.45;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRRKRRQKK 11
|||||
Db 47 YGRRKRRQRR 57

RESULT 6
S54381
tat protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
C:Accession: S54381
R:Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54381
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-86 <THE>
A:Cross-references: EMBL:M2639; NID:g329377; PIDN:AAA5363.1; PID:g329378
C:Genetics:
A:Introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator

Query Match 84.5%; Score 49; DB 2; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.45;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRRKRRQKK 11
|||||
Db 47 YGRRKRRQRR 57

RESULT 7
S33982
trans-activating transcription regulator - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Oct-1994 #sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
C:Accession: S33982; S26385; S19864
R:Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33982
A:Molecule type: DNA
A:Residues: 1-86 <CAR>
A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77625.1; PID:g60196
R:Siderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Erilte, H.; Sumner
Nucleic Acids Res. 20, 5311-5320, 1992
A:Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activato
A:Reference number: S26385; MUID:93065196
A:Accession: S26385
A:Molecule type: nucleic acid
A:Residues: 1-86 <SID>
A:Cross-references: EMBL:X64650; NID:g60144; PIDN:CAA5921.1; PID:g60145
C:Genetics:
A:Gene: tat
A:Introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency

Query Match 84.5%; Score 49; DB 2; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.45;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRORRKK 11
|||||
Db 47 YGRRKRORRR 57

RESULT 8
JC5591
transactivator protein - human immunodeficiency virus type 1

N:Alternate names: tat protein

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999

C:Accession: J05591

R:Hofmann, S.; Willbold, D.

Biochem. Biophys. Res. Commun. 235, 806-811, 1997

A:Title: A selection system to study protein-RNA interactions: Functional display of HIV

A:Reference number: J05591; MUID:97350867

A:Accession: J05591

A:Molecule type: protein

A:Residues: 1-86 <HO2>

C:Comment: This protein is a key regulatory protein in the viral replication cycle and is

F:22-31/Region: cysteine-rich

Query Match 84.5%; Score 49; DB 2; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.45;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRORRKK 11
|||||
Db 47 YGRRKRORRR 57

RESULT 9
T01665
tat protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000

C:Accession: T01665

R:Alison, M.; Main-Hobson, S.; Gluckman, J.C.; Sonigo, P.

Cell 46, 63-74, 1986

A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol

A:Reference number: Z14389; MUID:86245056

A:Accession: T01665

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-87 <ALI>

A:Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28015.1; PID:g60233

C:Genetics:

A:introns: 72/2

C:Superfamily: AIDS trans-activating transcription regulator

Query Match 84.5%; Score 49; DB 2; Length 87;
Best Local Similarity 72.7%; Pred. No. 0.46;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRORRKK 11
|||||
Db 47 YGRRKRORRR 57

RESULT 10
TNJ12

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Jul-1998

C:Accession: A04017

R:Araya, S.K.; Gallo, R.C.

Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986

A:Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity

A:Reference number: A94093; MUID:86177573

A:Accession: A04017

A:Molecule type: DNA

A:Residues: 1-95 <AKY>

C:Genetics:

A:Gene: tat

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 84.5%; Score 49; DB 1; Length 95;
Best Local Similarity 72.7%; Pred. No. 0.49;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRORRKK 11
|||||
Db 56 YGRRKRORRR 66

RESULT 11
E44001

trans-activating transcription regulator - human immunodeficiency virus type 1 (strain

N:Alternate names: tat protein

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jul-1998

C:Accession: E44001

R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6587-6600, 1992

A:Title: Complete nucleotide sequence, genome organization, and biological properties

A:Reference number: A44001; MUID:93021387

A:Accession: E44001

A:Molecule type: DNA

A:Residues: 1-101 <LIY>

A:Cross-references: GB:M93258

C:Genetics:

A:Gene: tat

A:introns: 72/2

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 84.5%; Score 49; DB 1; Length 101;
Best Local Similarity 72.7%; Pred. No. 0.52;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRORRKK 11
|||||
Db 47 YGRRKRORRR 57

RESULT 12
T09446

tat protein - human immunodeficiency virus type 1 (strain JRFL)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999

C:Accession: T09446

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazi

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09446

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-101 <PAN>

A:Cross-references: EMBL:U06362; NID:g1465777; PID:g1465783

C:Genetics:

A:Gene: tat

A:introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator

Query Match 84.5%; Score 49; DB 2; Length 101;
Best Local Similarity 72.7%; Pred. No. 0.52;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKKRRROKK 11
|||||
DB 47 YGKKRRRORR 57

RESULT 13

D38095
T-cell-specific transcription factor 1 splice form D - human
N:Alternate names: transcription factor TCF-ID
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 24-Sep-1999
C:Accession: D38095; S61877; S61800
R:van de Wetering, M.; Oosterwegel, M.; Holstege, F.; Dooyes, D.; Suijkerbuijk, R.; Geurts
J. Biol. Chem. 267, 8530-8536, 1992
A:Title: The human T cell transcription factor-1 gene. Structure, localization, and prom
A:Reference number: A38095; MUID:92235082
A:Accession: D38095

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <MAN>
A:Cross-references: GB:X63901
R:Mayr, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.
submitted to the EMBL Data Library, January 1995
A:Description: The human high mobility group (HMG)-box transcription factor TCF-1: novel

A:Reference number: S61877
A:Accession: S61877
A:Molecule type: mRNA
A:Residues: 1-250 <MAN>
A:Cross-references: EMBL:247361; NID:9619881; PTDN:CAA07439.1; PTD:9619882

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <MAN>
A:Cross-references: EMBL:247361; NID:9619881; PTDN:CAA07439.1; PTD:9619882
R:Mayr, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.

Biochim. Biophys. Acta 1263, 169-172, 1995
A:Title: The human high mobility group (HMG)-box transcription factor TCF-1: novel isofo
A:Reference number: S61796; MUID:95367594
A:Accession: S61800

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 244-250 <MAN>
A:Cross-references: EMBL:247361
C:Genetics:

A:introns: 32/3; 68/1; 97/2; 137/2; 191/3; 227/3; 243/3
C:Superfamily: unassigned HMG box proteins; HMG box homology
C:Keywords: alternative splicing; DNA binding; transcription factor
F:151-226/Domain: HMG box homology <HMG1>

Query Match 74.1%; Score 43; DB 2; Length 250;
Best Local Similarity 63.6%; Pred. No. 9.7;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YGKKRRROKK 11
|||||
DB 227 YGKKRRRSREK 237

RESULT 14

C38095
T-cell-specific transcription factor 1 splice form C - human
N:Alternate names: transcription factor TCF-1C
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 24-Sep-1999
C:Accession: C38095; S13449; S65007
R:van de Wetering, M.; Oosterwegel, M.; Holstege, F.; Dooyes, D.; Suijkerbuijk, R.; Geurts
J. Biol. Chem. 267, 8530-8536, 1992
A:Title: The human T cell transcription factor-1 gene. Structure, localization, and prom
A:Reference number: A38095; MUID:92235082

A:Accession: C38095
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <MAN>

A:Cross-references: GB:X63901
R:van de Wetering, M.; Oosterwegel, M.; Dooyes, D.; Clevers, H.
EMBO J. 10, 123-132, 1991
A:Title: Identification and cloning of TCF-1, a T lymphocyte-specific transcription f
A:Reference number: S13449; MUID:91114695
A:Accession: S13449

A:Molecule type: mRNA
A:Residues: 1-268 <MAN>
A:Cross-references: EMBL:X59871; NID:936789; PTDN:CAA42528.1; PTD:936790
A:Note: The authors describe an additional C-terminal exon of splice form C, which is
ences A38095 and S61796

R:Mayr, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.
Biochim. Biophys. Acta 1263, 169-172, 1995
A:Title: The human high mobility group (HMG)-box transcription factor TCF-1: novel is
A:Reference number: S61796; MUID:95367594
A:Accession: S65007

A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 244-268 <MAN>
A:Note: only a part of the coding sequence is given

C:Genetics:
A:introns: 32/3; 68/1; 97/2; 137/2; 191/3; 227/3 244/1
C:Superfamily: unassigned HMG box proteins; HMG box homology
C:Keywords: alternative splicing; DNA binding; transcription factor
F:151-226/Domain: HMG box homology <HMG1>

Query Match 74.1%; Score 43; DB 2; Length 268;
Best Local Similarity 63.6%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YGKKRRROKK 11
|||||
DB 227 YGKKRRRSREK 237

RESULT 15

A38095
T-cell-specific transcription factor 1 splice form A - human
N:Alternate names: transcription factor TCF-1A
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jul-2000
C:Accession: A38095; S16645; S65005
R:van de Wetering, M.; Oosterwegel, M.; Holstege, F.; Dooyes, D.; Suijkerbuijk, R.; G
J. Biol. Chem. 267, 8530-8536, 1992
A:Title: The human T cell transcription factor-1 gene. Structure, localization, and p
A:Reference number: A38095; MUID:92235082
A:Accession: A38095

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-269 <MAN>
A:Cross-references: EMBL:X59869; NID:936791; PTDN:CAA56795.1; PTD:96006565
A:Note: authors translated the codon GAT for residue 253 as Ser

R:van de Wetering, M.; Oosterwegel, M.; Dooyes, D.; Clevers, H.
EMBO J. 10, 123-132, 1991
A:Title: Identification and cloning of TCF-1, a T lymphocyte-specific transcription f
A:Reference number: S13449; MUID:91114695
A:Accession: S16645

A:Molecule type: mRNA
A:Residues: 1-269 <MAN>
A:Cross-references: EMBL:X59869; NID:936785; PTDN:CAA42526.1; PTD:936786
R:Mayr, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.
Biochim. Biophys. Acta 1263, 169-172, 1995

A:Title: The human high mobility group (HMG)-box transcription factor TCF-1: novel is
A:Reference number: S61796; MUID:95367594
A:Accession: S65005
A:Status: not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 244-269 <MAN>

C:Genetics:
 A:introns: 32/3; 68/1; 97/2; 137/2; 191/3; 227/3; 244/1
 C:Superfamily: unassigned HMG box proteins; HMG box homology
 C:Keywords: alternative splicing; DNA binding; transcription factor
 F;151-226/Domain: HMG box homology <HMG1>

Query Match	74.1%;	Score 43;	DB 2;	length 269;
Best Local Similarity	63.6%;	Pred. No. 10;		
Matches	7;	Conservative	3;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	1 YGRRRRRQKK	11		
	: ::			
Db	227 YGKKRRSREK	237		

Search completed: July 15, 2002, 13:01:03
 Job time: 469 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:23:33 ; Search time 44.9 Seconds
(without alignments)
9.486 Million cell updates/sec

Title: US-09-712-819A-8
Perfect score: 58
Sequence: 1 YGKKRRQKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	89.7	86	1	TAT_HVIND
2	49	84.5	86	1	TAT_HV1B5
3	49	84.5	86	1	TAT_HV112
4	49	84.5	86	1	TAT_HV1B1
5	49	84.5	86	1	TAT_HV1BR
6	49	84.5	86	1	TAT_HV1H2
7	49	84.5	86	1	TAT_HV1PV
8	49	84.5	86	1	TAT_HV1Z2
9	49	84.5	86	1	TAT_HV1Z6
10	49	84.5	87	1	TAT_HV1MA
11	49	84.5	101	1	TAT_HV1A2
12	49	84.5	101	1	TAT_HV1C4
13	49	84.5	101	1	TAT_HV1JR
14	49	84.5	101	1	TAT_HV1MN
15	49	84.5	101	1	TAT_HV1OY
16	49	84.5	101	1	TAT_HV1S1
17	49	84.5	101	1	TAT_HV1SC
18	49	84.5	101	1	TAT_HV1Y2
19	48	82.8	101	1	TAT_HV1S3
20	47	81.0	99	1	TAT_HV1EL
21	47	81.0	102	1	TAT_HV1RH
22	43	74.1	269	1	TCFL_HUMAN
23	43	74.1	303	1	TCFL_MOUSE
24	43	74.1	1022	1	ALAI_ANGAN
25	42	72.4	128	1	RS12_AQUAE
26	42	72.4	431	1	DBP8_YEAST
27	42	72.4	552	1	DIOL_MOUSE
28	41	70.7	397	1	LEFL_MOUSE
29	41	70.7	397	1	LEFL_RAT
30	41	70.7	399	1	LEFL_HUMAN
31	41	70.7	787	1	SMO_HUMAN
32	41	70.7	793	1	SMO_MOUSE
33	41	70.7	793	1	SMO_RAT

34	39	67.2	148	1	Y18K_MSYS	P14989 maize strea
35	39	67.2	153	1	Y18K_MSYN	P14978 maize strea
36	39	67.2	643	1	SYRM_YEAST	P38714 saccharomyc
37	39	67.2	747	1	KE3B_HUMAN	O15066 homo sapien
38	39	67.2	747	1	KE3B_MOUSE	O61771 mus musculu
39	38	65.5	144	1	YHP5_YEAST	P38808 saccharomyc
40	38	65.5	478	1	AMP2_HUMAN	P50579 homo sapien
41	38	65.5	478	1	AMP2_MOUSE	O08663 mus musculu
42	38	65.5	478	1	AMP2_RAT	P38062 rattus norv
43	38	65.5	794	1	SMO_CHICK	O42224 gallus gall
44	38	65.5	999	1	MFD_HELPJ	O26066 hellicodact
45	38	65.5	1001	1	MFD_HELPJ	Q92357 hellicodact

ALIGNMENTS

```

RESULT 1
TAT_HVIND STANDARD; PRT; 86 AA.
ID TAT_HVIND
AC P18804:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (NKK isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11695;
RN [1]
RP MEDLINE=90034200; PubMed=2806917;
RX Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F.,
RA Hampe A., Chermann J.C., Rey F., Barre-Sinoussi F., Galibert F.,
RT "Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the
RL Gene 81:275-284(1989)".
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC -1- TRANSCRIPTION RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC -1- ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -1- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH
CC AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
CC -----
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CC -----
CC EMBL: M27323; AAA4866.1; -.
CC PIR: J00071; TNLJND.
CC DR HIV; M27323; TAT$NDK.
CC DR InterPro: IPR001831; HIV_Tat.
CC DR Pfam: PF00539; Tat; 1.
CC DR PRINTS: PR00055; HIVTANDOMAIN.
CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 86 AA; 9711 MW; 7DB9E64E0AE8B0F4 CRC64;

```

Query Match 89.7%; Score 52; DB 1; Length 86;
Best Local Similarity 81.8%; Pred. No. 0.024;
Matches 9; Conservative 2; Indels 0; Gaps 0;

Y 1 YGKKRRQKK 11
| | | | | | | | | |
D 47 YGKKRRQRRK 57

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RESULT 2
TAT_HV1B5 STANDARD: PRT: 58 AA.
AC P04612;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (BHS isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Pappas T.S., Chrayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT *Complete nucleotide sequence of the AIDS virus, HTLV-III.*;
RL Nature 313:277-284(1985).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
-----
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-----
DR EMBL: K02012; AAA44656.1; -.
DR HIV: K02012; TATSBH5.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
PT NON_TER
KW SEQUENCE 58 AA: 6800 MW: E36C21F8FED81E3 CRC64;
SQ
Query Match 84.5%; Score 49; DB 1; Length 58;
Best Local Similarity 72.7%; Pred. No. 0.05;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 YGKRRRQKK 11
DB 47 YGKRRRQRR 57

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RT "Three novel genes of human T-lymphotropic virus type III: immune
RT reactivity of their products with sera from acquired immune
RT deficiency syndrome patients.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
-----
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-----
DR EMBL: M1840; AAA4499.1; -.
DR PIR: A04017; TNLJ12.
DR HIV: M1840; TATSPCV12.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
PT SEQUENCE 86 AA: 9758 MW: 4DD609414FBE9115 CRC64;
SQ
Query Match 84.5%; Score 49; DB 1; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.074;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 YGKRRRQKK 11
DB 47 YGKRRRQRR 57

```

```

CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -1- MISCELLANEOUS: THE TWO ISOLATES TAR SEQUENCE ARE IDENTICAL.
CC -----
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CC -----
DR EMBL: M14100; AAA44676.1; -
DR EMBL: M15654; AAA44199.1; -
DR HIV: M15654; TATSHB102.
DR HIV: M14100; TATSHXB3.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA; 9784 MW; 4DD609415FAF9015 CRC64;

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Query Match      84.5%; Score 49; DB 1; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.074;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGKKRRRQKK 11
Db 47 YGKKRRRQRR 57

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RESULT 5
TAT_HVI1B1R STANDARD; PRT; 86 AA.
AC P04610;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAR protein (transactivating regulatory protein).
GN TAR.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-8509333; PubMed-2981635;
RT Wain-Hobson S., Sonigo P., Dancos O., Cole S., Allzon M.;
RL "Nucleotide sequence of the AIDS virus, LAV."
RL Cell 40:9-17(1985).
RP SEQUENCE FROM N.A. (CLONE PML4-3).
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL Submitted (JUN-1988) to the EMBL/Genbank/DDJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----

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DR EMBL: K02013; AAB59745.1; -
DR EMBL: M19921; AAA44985.1; -
DR HIV: K02013; TATSBRO.
DR HIV: M19921; TATSNM43.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT VARIANT 24 24 T -> N (IN CLONE PML4-3).
FT VARIANT 39 39 T -> M (IN CLONE PML4-3).
FT VARIANT 58 61 PPOG -> AHON (IN CLONE PML4-3).
FT VARIANT 67 67 V -> A (IN CLONE PML4-3).
FT VARIANT 77 77 P -> S (IN CLONE PML4-3).
SQ SEQUENCE 86 AA; 9769 MW; 9B1B4A915FAF8A14 CRC64;

```

```

Query Match      84.5%; Score 49; DB 1; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.074;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGKKRRRQKK 11
Db 47 YGKKRRRQRR 57

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```

RESULT 6
TAT_HVI1H2 STANDARD; PRT; 86 AA.
AC P04608; O09778;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAR protein (transactivating regulatory protein).
GN TAR.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87299196; PubMed-3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RL Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RL virus."
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RL Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/Genbank/DDJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
DR EMBL: K03455; AAB50256.1; -
DR EMBL: AF033819; AAC82591.1; -
DR HIV: K03455; TATSHXB2.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Transcription regulation; Activator; RNA-binding; Nuclear protein;

```

KM AIDS.
SQ SEQUENCE 86 AA: 9837 MW: 4DDC56D979769115 CRC64:

Query Match 84.5%; Score 49; DB 1; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.074;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRROKK 11
|||||
DB 47 YGRRKRRORR 57

RESULT 7

TAT_HV1P STANDARD; PRT; 86 AA.
AC P04607;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).

CC -I- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -I- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

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CC EMBL: K02083; AAB59870.1; -;
DR EMBL: X01762; -; NOT_ANNOTATED_CDS.
DR HIV: K02083; TATSPV22.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA: 9794 MW: 4DD5C6415FAF9015 CRC64:

Query Match 84.5%; Score 49; DB 1; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.074;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRROKK 11
|||||
DB 47 YGRRKRRORR 57

RESULT 8

TAT_HV126 STANDARD; PRT; 86 AA.
ID TAT_HV126
AC P12506;
DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]

RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.

CC -I- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -I- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

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CC EMBL: M2639; AAA45363.1; -;
DR HIV: M2639; TAT8226.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA: 9737 MW: 97561D72AFCFF19 CRC64:

Query Match 84.5%; Score 49; DB 1; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.074;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRROKK 11
|||||
DB 47 YGRRKRRORR 57

RESULT 9

TAT_HV126 STANDARD; PRT; 86 AA.
AC P04609;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; PubMed=3036660;
RA Sriivasan A., Anand R., York D., Ranganathan P., Feorino P.,
RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
RA Sanchez-Pescador R.;

RT "Molecular characterization of human immunodeficiency virus from
RT Zaire: nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene.";
RL Gene 52:71-82(1987).

CC -I- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -I- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

```
CC -----
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CC -----
DR EMBL: K03458; AAA45377.1; -.
DR PIR: C26192; TNLJZR.
DR HIV: K03458; TAT526.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA; 9736 MW; E1E0AD741FCFF5AC CRC64;

Query Match
Best Local Similarity 84.5%; Score 49; DB 1; Length 86;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKKRRRQKK 11
Db 47 YGKKRRRQRR 57

RESULT 10
TAT_HV1A STANDARD; PRT; 87 AA.
ID TAT_HV1A
AC P04613;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tat protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11697;
RN [1]
RP MEDLINE=86245056; PubMed=2424612;
RA Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.";
RT Cell 46:63-74(1986)
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANSCRIPTING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
DR EMBL: X04415; CAA28015.1; -.
DR HIV: K03456; TAT5MAL.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 87 AA; 10036 MW; 3832412849D5BICE CRC64;
```

```
Query Match
Best Local Similarity 84.5%; Score 49; DB 1; Length 87;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKKRRRQKK 11
Db 47 YGKKRRRQRR 57

RESULT 11
TAT_HV1A2 STANDARD; PRT; 101 AA.
ID TAT_HV1A2
AC P04614;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tat protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
RT (ARV-2).";
RT Science 227:484-492(1985).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANSCRIPTING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
DR EMBL: K02007; AAB59879.1; -.
DR HIV: K02007; TAT5SF2.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 101 AA; 11557 MW; 1762370A3BD641PD CRC64;

Query Match
Best Local Similarity 84.5%; Score 49; DB 1; Length 101;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKKRRRQKK 11
Db 47 YGKKRRRQRR 57

RESULT 12
TAT_HV1C4 STANDARD; PRT; 101 AA.
ID TAT_HV1C4
AC P05907;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tat protein (Transactivating regulatory protein).
GN TAT.
```

```

OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
CC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID-11687;
RN
  (1)
  SEQUENCE FROM N.A.
RX MEDLINE-87041461; PubMed-3490666;
RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
RA Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genomic sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13137; AAA44309.1; -.
DR PIR: B25523; TNLJH4.
DR HIV: M13137; TATSCDC45.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Transcription regulation; Activator; RNA-binding; Nuclear protein;
KM AIDS.
SQ SEQUENCE 101 AA; 11594 MW; 817D915F3FB1C7FA CRC64;

Query Match
Best Local Similarity 84.5%; Score 49; DB 1; Length 101;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRRQKK 11
  |||||
DB 47 YGKRRRQRR 57

RESULT 13
TAT_HV1JR STANDARD; PRT; 101 AA.
ID TAT_HV1JR
AC P20879;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID-11688;
RN
  (1)
  SEQUENCE FROM N.A.
RX Koyanagi S., Chen I.S.Y.;
RA Submitted (DEC-1988) to the HIV data bank.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
DR EMBL: M38429; -; NOT_ANNOTATED_CDS.
DR HIV: M38429; TAT5JRCFSF.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Transcription regulation; Activator; RNA-binding; Nuclear protein;
KM AIDS.
SQ SEQUENCE 101 AA; 11508 MW; 36CBDBFF7F8D4FA CRC64;

Query Match
Best Local Similarity 84.5%; Score 49; DB 1; Length 101;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRRQKK 11
  |||||
DB 47 YGKRRRQRR 57

RESULT 14
TAT_HV1MN STANDARD; PRT; 101 AA.
ID TAT_HV1MN
AC P05905;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID-11696;
RN
  (1)
  SEQUENCE FROM N.A.
RX MEDLINE-88219542; PubMed-3369091;
RA Gungo C., Guo H.-G., Franchini G., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S., Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC -----
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CC -----
DR EMBL: M17449; AAA44851.1; -.
DR HIV: M17449; TAT5MN.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Transcription regulation; Activator; RNA-binding; Nuclear protein;
KM AIDS.
SQ SEQUENCE 101 AA; 11634 MW; 2DBC7A21486389FF CRC64;

Query Match
Best Local Similarity 84.5%; Score 49; DB 1; Length 101;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```


QY 1 YGRRRRRQKK 11
 |||||
 Db 47 YGRRRRRQRR 57

RESULT 15
 TAT_HV10Y

ID TAT_HV10Y STANDARD; PRT; 101 AA.
 AC P20893;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE TAT protein (Transactivating regulatory protein).
 GN TAT.
 OS Human immunodeficiency virus type 1 (OY1 isolate) (HIV-1).
 OC Viruses; Retrovirdae; Lentivirus.
 OX NCBI_TaxID=11699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148544; PubMed=2559749;
 RA Huet T., Dazza M.C., Brun-Vesinet F., Roelants G.E., Main-Hobson S.;
 RT "A highly defective HIV-1 strain isolated from a healthy gabonese
 individual presenting an atypical western blot.";
 RL AIDS 3:707-715(1989).
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
 CC -1- MISCELLANEOUS: THE OY1 ISOLATE WAS TAKEN FROM THE BLOOD OF A
 CC HEALTHY GABONESE INDIVIDUAL.
 CC -1- MISCELLANEOUS: THE SINGLE C -> S SUBSTITUTION AT RESIDUE 22 OF THE
 CC OY1 TAT PROTEIN RENDERS IT INACTIVE, BUT MAY NOT ACCOUNT FOR THE
 CC AVIRULENCE OF THE VIRUS.
 CC -----
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 CC -----
 CC EMBL: M26727; AA83395.1; -.
 CC HIV: M26727; TATSOYI.
 CC InterPro: IPR001831; HIV_Tat.
 CC Pfam: PF00539; Tat; 1.
 CC PRINTS: PR00055; HIVTATDOMAIN.
 CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
 CC AIDS.
 SO SEQUENCE 101 AA; 11561 MW; 83ACAC36CC4C87AD CRC64;

Query Match 84.5%; Score 49; DB 1; Length 101;
 Best Local Similarity 72.7%; Pred. No. 0.087;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YGRRRRRQKK 11
 |||||
 Db 47 YGRRRRRQRR 57

Search completed: July 15, 2002, 13:23:34
 Job time: 1450 sec

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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:22:47 ; Search time 172.49 Seconds
(without alignments)
11.032 Million cell updates/sec

Title: US-09-712-819A-8
Perfect score: 58
Sequence: 1 YGRRKKRQKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	89.7	72	15	099AP9 human immun
2	52	89.7	72	15	099AP7 human immun
3	52	89.7	72	15	099AP6 human immun
4	52	89.7	72	15	099AP5 human immun
5	52	89.7	72	15	099AP3 human immun
6	52	89.7	72	15	099AP2 human immun
7	52	89.7	72	15	099AN9 human immun
8	52	89.7	72	15	099AN8 human immun
9	52	89.7	72	15	099AN7 human immun
10	52	89.7	72	15	086025 human immun
11	52	89.7	72	15	075573 human immun
12	52	89.7	72	15	075574 human immun
13	52	89.7	72	15	P90144 human immun
14	52	89.7	101	15	09YK33 human immun
15	52	89.7	101	15	0902K3 human immun
16	49	84.5	65	15	075540 human immun

17	49	84.5	65	15	075544 human immun
18	49	84.5	71	15	0910M7 human immun
19	49	84.5	71	15	0910M6 human immun
20	49	84.5	71	15	0910M5 human immun
21	49	84.5	71	15	0910M4 human immun
22	49	84.5	71	15	0910M3 human immun
23	49	84.5	71	15	0910M2 human immun
24	49	84.5	71	15	0910M1 human immun
25	49	84.5	71	15	0910M0 human immun
26	49	84.5	71	15	0910L9 human immun
27	49	84.5	71	15	0910L8 human immun
28	49	84.5	71	15	0910L7 human immun
29	49	84.5	71	15	0910L6 human immun
30	49	84.5	71	15	0910L5 human immun
31	49	84.5	71	15	0910L4 human immun
32	49	84.5	71	15	0910L3 human immun
33	49	84.5	71	15	0910L2 human immun
34	49	84.5	71	15	0910L1 human immun
35	49	84.5	71	15	0910L0 human immun
36	49	84.5	71	15	0910K9 human immun
37	49	84.5	71	15	0910K7 human immun
38	49	84.5	71	15	0910K6 human immun
39	49	84.5	71	15	0910K5 human immun
40	49	84.5	71	15	0910K4 human immun
41	49	84.5	71	15	0910K3 human immun
42	49	84.5	71	15	0910K2 human immun
43	49	84.5	71	15	0910K1 human immun
44	49	84.5	71	15	0910K0 human immun
45	49	84.5	71	15	040224 human immun

ALIGNMENTS

RESULT 1
099AP9 PRELIMINARY; PRT; 72 AA.
ID 099AP9
AC 099AP9;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PAIRD, MOTHER;
RA MEDLINE-21322025; PubMed-11429117;
RX Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;
RT "Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission.";
RL AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007056; AAG32103.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA: 8342 MW: 603G524B7D9F2A6F CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;
Best Local Similarity 81.8%; Pred No. 0.032;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 YGRRKKRQKK 11
|||||:::

DB 47 YGKRRRRQRRK 57

RESULT 2

ID 099AP7 PRELIMINARY; PRT: 72 AA.

AC 099AP7; MEDLINE-21322025; PubMed-11429117;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).

GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID-11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-PAIRD, MOTHER;

RX MEDLINE-21322025; PubMed-11429117;

RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;

RT "Characterization of HIV Type 1 tat Sequences Associated with Perinatal Transmission."

RT Perinatal Transmission."

RT AIDS Res. Hum. Retroviruses 17:765-773(2001).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).

CC EMBL: AY007058; AAC32105.1; -.

DR Interpro: IPR001831; HIV_Tat.

DR Pfam: PF00539; Tat. 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

KW Activator; Nuclear protein; RNA-binding; Transcription regulation.

FT NON_TER 72

SQ SEQUENCE 72 AA; 8342 MW; 603C524B7D9F2A8F CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;

Best Local Similarity 81.8%; Pred. No. 0.032;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKRRRRQRRK 11

DB 47 YGKRRRRQRRK 57

RESULT 3

ID 099AP6 PRELIMINARY; PRT: 72 AA.

AC 099AP6; MEDLINE-21322025; PubMed-11429117;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).

GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID-11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-PAIRD, MOTHER;

RX MEDLINE-21322025; PubMed-11429117;

RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;

RT "Characterization of HIV Type 1 tat Sequences Associated with Perinatal Transmission."

RT Perinatal Transmission."

RT AIDS Res. Hum. Retroviruses 17:765-773(2001).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).

CC EMBL: AY007059; AAC32106.1; -.

DR Interpro: IPR001831; HIV_Tat.

DR Pfam: PF00539; Tat. 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

DR PRINTS: PR00055; HIVTATDOMAIN.

KW Activator; Nuclear protein; RNA-binding; Transcription regulation.

FT NON_TER 72

SQ SEQUENCE 72 AA; 8342 MW; 603C524B7D9F2A8F CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;

Best Local Similarity 81.8%; Pred. No. 0.032;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKRRRRQRRK 11

DB 47 YGKRRRRQRRK 57

RESULT 4

ID 099AP5 PRELIMINARY; PRT: 72 AA.

AC 099AP5; MEDLINE-21322025; PubMed-11429117;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).

GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID-11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-PAIRD, MOTHER;

RX MEDLINE-21322025; PubMed-11429117;

RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;

RT "Characterization of HIV Type 1 tat Sequences Associated with Perinatal Transmission."

RT Perinatal Transmission."

RT AIDS Res. Hum. Retroviruses 17:765-773(2001).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).

CC EMBL: AY007060; AAC32107.1; -.

DR Interpro: IPR001831; HIV_Tat.

DR Pfam: PF00539; Tat. 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

KW Activator; Nuclear protein; RNA-binding; Transcription regulation.

FT NON_TER 72

SQ SEQUENCE 72 AA; 8352 MW; 766EC9318D9F2A8F CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;

Best Local Similarity 81.8%; Pred. No. 0.032;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKRRRRQRRK 11

DB 47 YGKRRRRQRRK 57

RESULT 5

ID 099AP3 PRELIMINARY; PRT: 72 AA.

AC 099AP3; MEDLINE-21322025; PubMed-11429117;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).

GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID-11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-PAIRD, MOTHER;

RX MEDLINE-21322025; PubMed-11429117;

RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;

RT "Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission."
RL AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007062; AAC32109.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA; 8355 MW; EF68655B4D8FC481 CRC64;

QY 1 YGKRRRQKK 11
|||||:|
Db 47 YGKRRRQRRK 57

Query Match 89.7%; Score 52; DB 15; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.032;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
Q99AP2 PRELIMINARY; PRT; 72 AA.
ID Q99AP2;
AC Q99AP2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PAIRD, MOTHER;
RX MEDLINE-21322025; PubMed-11429117;
RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;
RT "Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission."
RL AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007063; AAC32110.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA; 8342 MW; 603C524B7D9F2A8F CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.032;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRRQKK 11
|||||:|
Db 47 YGKRRRQRRK 57

RESULT 7
Q99AN9 PRELIMINARY; PRT; 72 AA.
ID Q99AN9;
AC Q99AN9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PAIRD, MOTHER;
RX MEDLINE-21322025; PubMed-11429117;
RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;
RT "Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission."
RL AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007066; AAC32113.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA; 8340 MW; 767E273F7D9F2A8F CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.032;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRRQKK 11
|||||:|
Db 47 YGKRRRQRRK 57

RESULT 8
Q99AN8 PRELIMINARY; PRT; 72 AA.
ID Q99AN8;
AC Q99AN8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PAIRD, MOTHER;
RX MEDLINE-21322025; PubMed-11429117;
RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;
RT "Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission."
RL AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007067; AAC32114.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA; 8352 MW; 766EC9318D9F2A8F CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.032;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRORRKK 11
|||||||:|
DB 47 YGRRKRRORRKK 57

RESULT 9

O99AN7 PRELIMINARY: PRT: 72 AA.
ID O99AN7
AC O99AN7
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIONAL REGULATORY PROTEIN) (FRAGMENT).
GN TAT
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirda; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAIRD, MOTHER.
RX MEDLINE=21322025; PubMed=11429117;
RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;
RT "Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission.";
RL AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007068; AAC32115.1; -;
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat. 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA: 8342 MW: 603524B7D9F2A8F CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.032;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRORRKK 11
|||||||:|
DB 47 YGRRKRRORRKK 57

RESULT 10
O86025 PRELIMINARY: PRT: 72 AA.
ID O86025
AC O86025
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIONAL REGULATORY PROTEIN) (FRAGMENT).
GN TAT
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirda; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95032920; PubMed=7946099;
RA Sabino E., Pan L.Z., Cheng-Mayer C., Mayer A.;
RT "Comparison of in vivo plasma and peripheral blood mononuclear cell
RT HIV-1 quasi-species to short-term tissue culture isolates: an analysis
RT of tat and C2-V3 env regions.";
RL AIDS 8:901-909(1994).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: U01437; AA57782.1; -;
DR InterPro: IPR001831; HIV_Tat.

DR Pfam: PF00539; Tat. 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA: 8406 MW: 7598236E9FDEB737 CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.032;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRORRKK 11
|||||||:|
DB 47 YGRRKRRORRKK 57

RESULT 11

O75573 PRELIMINARY: PRT: 72 AA.
ID O75573
AC O75573
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIONAL REGULATORY PROTEIN) (FRAGMENT).
GN TAT
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirda; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T10;
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RT "The TAT and C2-V3 Envelope Genes in the Molecular Epidemiology of
RT Human Immunodeficiency Virus-1.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: U57281; AB17841.1; -;
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat. 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA: 8306 MW: D3E50D0E0BDF2E CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.032;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRORRKK 11
|||||||:|
DB 47 YGRRKRRORRKK 57

RESULT 12

O75574 PRELIMINARY: PRT: 72 AA.
ID O75574
AC O75574
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIONAL REGULATORY PROTEIN) (FRAGMENT).
GN TAT
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirda; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T10;

RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
 RT "The TAR and C2-V3 Envelope Genes in the Molecular Epidemiology of
 Human Immunodeficiency Virus-1."
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANSCRIPTONAL REGULATOR SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER (BY SIMILARITY).
 DR EMBL: U57282; AAB17842.1; -.
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat.1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
 FT NON_TER 1 1
 FT NON_TER 72 72
 SQ SEQUENCE 72 AA; 8344 MW; D3E5040DE0FCF2E CMC64;

Query Match 89.7%; Score 52; DB 15; Length 72;
 Best Local Similarity 81.8%; Pred. No. 0.032;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRRQKK 11
 DB 47 YGKRRRQKK 57

RESULT 13
 P90144 PRELIMINARY; PRT; 72 AA.
 AC P90144;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE TAR PROTEIN (TRANSCRIPTIVATING REGULATOR PROTEIN) (FRAGMENT).
 GN TAR.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT WCP1R;
 RX MEDLINE-99049627; PubMed-9833881;
 RA Quiñones-Mateu M.E., Mas A., Lain de Lera T., Soriano V., Alcamí J.,
 RA Lèderman M.M., Domingo E.;
 RT "LTR and tat variability of HIV-1 isolates from patients with
 RT divergent rates of disease progression."
 RL Virus Res. 57:11-20(1998).
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANSCRIPTONAL REGULATOR SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER (BY SIMILARITY).
 DR EMBL: U80540; AAC82979.1; -.
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat.1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
 FT NON_TER 72 72
 FT NON_TER 72 72
 SQ SEQUENCE 72 AA; 8284 MW; 730494F201B6B58C CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;
 Best Local Similarity 81.8%; Pred. No. 0.032;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRRQKK 11
 DB 47 YGKRRRQKK 57

RESULT 14
 Q9YP33 PRELIMINARY; PRT; 101 AA.

AC Q9YP33;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE TAR PROTEIN (TRANSCRIPTIVATING REGULATOR PROTEIN).
 GN TAR.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT WCP1R;
 RA Fang G., Weiser B., Chappey C., Vlasosky A., Townsend L., Wang Q.,
 RA Burger H.;
 RT "Complete Plasma HIV-1 Sequence: Spi-Promoter Deletion Can Lead to
 RT Non-Progressive Infection."
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANSCRIPTONAL REGULATOR SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER (BY SIMILARITY).
 DR EMBL: U69591; AAD10925.1; -.
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat.1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
 SQ SEQUENCE 101 AA; 11445 MW; 1190630EAF15ADB CMC64;

Query Match 89.7%; Score 52; DB 15; Length 101;
 Best Local Similarity 81.8%; Pred. No. 0.045;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRRQKK 11
 DB 47 YGKRRRQKK 57

RESULT 15
 Q902K3 PRELIMINARY; PRT; 101 AA.
 AC Q902K3;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE TAR PROTEIN.
 GN TAR.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ARMA185;
 RA Carr J.K., Avila M., Gomez-Carrillo M., Salomon H., Hierholzer J.,
 RA Watanaveeradej V., Pando M., Negrete M., Russell K.L., Sanchez J.,
 RA Birx D.L., Andrade R., Vinolas J., McCutchan F.E.;
 RT "Diverse BF Recombinants have spread widely since the introduction of
 RT HIV-1 into South America."
 RL AIDS 0:0-0(2001).
 SQ SEQUENCE 101 AA; 11525 MW; 52A6782BF08FAAB9 CRC64;

Query Match 89.7%; Score 52; DB 15; Length 101;
 Best Local Similarity 81.8%; Pred. No. 0.045;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRRQKK 11
 DB 47 YGKRRRQKK 57

Search completed: July 15, 2002, 13:22:47
Job time: 1483 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:57:58 ; Search time 228.39 Seconds
(without alignments)
5.350 Million cell updates/sec

Title: US-09-712-819A-8
Perfect score: 58
Sequence: 1 YGRKKRRQKK 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.GeneSeq_032802:*

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- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	89.7	11	22	AAU09906 Interleukin 17 (hi
2	52	89.7	86	11	AA09303 Sequence deduced f
3	49	84.5	11	19	AAW50263 HIV-1 tat protein.
4	49	84.5	11	20	AAV25075 TAT transduction d
5	49	84.5	11	20	AAV05415 Tat peptide. Unid
6	49	84.5	11	21	AAAB03932 Minimal eleven ami
7	49	84.5	11	21	AAAB03961 Beta-catenin deriv
8	49	84.5	11	21	AAAB27088 Peptide associated
9	49	84.5	11	21	AAAB3698 HIV TAT transducti
10	49	84.5	11	21	AAAB39413 HIV tat protein tr
11	49	84.5	11	21	AAAB09907

12	49	84.5	11	21	AAV93542 Amino acid sequenc
13	49	84.5	11	21	AAV71015 Human immunodefici
14	49	84.5	11	22	AAU09932 Human immunodefici
15	49	84.5	11	22	AAU09812 HIV-1 tat protein
16	49	84.5	11	22	AAE13064 Protein transducti
17	49	84.5	11	22	AAE12891 Human immunodefici
18	49	84.5	11	22	AAE12891 HIV tat protein fr
19	49	84.5	11	22	AAE12891 HIV-1 tat protein
20	49	84.5	11	22	AAE12605 Human immunodefici
21	49	84.5	11	22	AAE12204 Membrane transport
22	49	84.5	11	22	AAE12204 Internealing pept
23	49	84.5	11	22	AAE12204 HIV TAT protein tr
24	49	84.5	11	22	AAE12204 HIV-1 tat protein
25	49	84.5	11	22	AAE12204 Human immunodefici
26	49	84.5	11	22	AAE12204 Human immunodefici
27	49	84.5	11	22	AAE12204 HIV TAT peptide tr
28	49	84.5	11	22	AAE12204 Human immunodefici
29	49	84.5	11	22	AAE12204 Protein transducti
30	49	84.5	11	22	AAE12204 HIV tat protein tr
31	49	84.5	11	22	AAE12204 Protein transducti
32	49	84.5	11	22	AAE12204 Human Chk1 kinase
33	49	84.5	11	22	AAE12204 Human G2 checkpoint
34	49	84.5	11	22	AAE12204 Transduction doma
35	49	84.5	11	22	AAE12204 HIV-1 TAT protein
36	49	84.5	11	22	AAE12204 HIV tat protein tr
37	49	84.5	11	22	AAE12204 HIV TAT protein tr
38	49	84.5	11	22	AAE12204 HIV TAT protein tr
39	49	84.5	11	22	AAE12204 HIV TAT protein tr
40	49	84.5	11	22	AAE12204 HIV TAT protein tr
41	49	84.5	11	22	AAE12204 HIV TAT protein tr
42	49	84.5	11	22	AAE12204 HIV TAT protein tr
43	49	84.5	11	22	AAE12204 HIV TAT protein tr
44	49	84.5	11	22	AAE12204 HIV TAT protein tr
45	49	84.5	11	22	AAE12204 HIV TAT protein tr

ALIGNMENTS

AAU09906	1	AAU09906 standard; Protein; 11 AA.	
XX	XX	AAU09906:	
XX	XX	14-FEB-2002 (first entry)	
XX	XX	Interleukin 17 (hIL-17) receptor like protein associated peptide #1.	
DE	XX	Interleukin 17: hIL-17 receptor like protein; immunomodulatory;	
KW	XX	anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;	
KW	XX	hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;	
KW	XX	anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;	
KW	XX	vascular; cytostatic; anti-leukemic; anti-interleukin; ophthalmological;	
KW	XX	hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;	
KW	XX	bone disease; vascular disorder; eye disorder; cancer; human.	
XX	OS	Synthetic.	
XX	XX	WO200168859-A2.	
XX	XX	20-SEP-2001.	
XX	XX	15-MAR-2001; 2001WO-US08678.	
XX	XX	16-MAR-2000; 2000US-189816P.	
XX	XX	28-NOV-2000; 2000US-0724460.	
XX	XX	(AMGE-) AMGEN INC.	
XX	XX	Jing S;	
XX	XX	WPI; 2001-611392/70.	

```

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
PT diabetes, psoriasis and glaucoma -
XX
XX PS Disclosure; Page 149; 158pp; English.
XX
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
CC receptor like polypeptides useful as vaccines and in gene therapy. These
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
CC osteoprotic, vascular, cytostatic, anti-leukaemic, anti-infectivity and
CC ophthalmological activities. The IL-17 receptor like nucleic acids and
CC proteins may be used to prevent and treat diseases associated with
CC inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
CC include, for example immune disorders (e.g. inflammation, diabetes and
CC transplant rejection), infections (e.g. hepatitis and septicemia),
CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC DNA and its complements may also used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rp may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The
CC anti-IL17rp antibodies and antagonists may also be used to down regulate
CC expression and activity.
CC Note: This artificial peptide sequence is given in the sequence listing
CC but is not described in the specification.
XX
XX SQ Sequence 11 AA:
XX
XX Query Match 89.7%; Score 52; DB 22; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 0.042;
XX Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YGRRKKRRQKK 11
XX |||||:|
XX Db 1 ygrrkkrrgrrk 11
XX
XX RESULT 2
XX AAR09303
XX ID AAR09303 standard; protein; 86 AA.
XX
XX AC AAR09303;
XX
XX XX 27-FEB-1991 (first entry)
XX
XX DE Sequence deduced from tat gene of HIV 1-NDK.
XX
XX KW Human immunodeficiency virus; AIDS.
XX
XX OS HIV 1-NDK.
XX
XX XX
XX FH Key Location/Qualifiers
XX FT 1..72
XX FT /label= tat ex2
XX FT 73..86
XX FT /label= tat ex3
XX
XX WO9013630-A.
XX
XX PN
XX XX
XX PD 15-NOV-1990.
XX
XX PF 02-MAY-1990; 90WO-FR00312.

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XX
XX 03-MAY-1989; 89FR-0005914.
XX
XX PA (INRM ) INSERM INST NAT SANTE.
XX
XX P1 Barre-Sinoussi F, Chermann JC, Devaux C, Rey F, Sire J;
XX P1 Spire B;
XX
XX DR WPI; 1990-361470/48.
XX DR N-PSDB; AA006635.
XX
XX PT New HIV-NDK retrovirus and protein component - used in vaccines
XX PT against Immuno-deficiency disorders and in raising MAbs for
XX PT retro-virus detection in vivo.
XX
XX PS Disclosure; Fig 2; 37pp; French.
XX
XX CC The HIV NDK virus was isolated from peripheral blood lymphocytes of
XX CC an AIDS patient. A genomic library was prepd. from DNA extracted
XX CC from CEM cells infected with the virus. The library was screened
XX CC with a pMT1 probe corresp. to a fragment from HIV 1. The virus is
XX CC more cytopathic than other strains and is not inhibited by OKT4A.
XX CC It has been deposited as CNCM I-857. The sequence can be used to
XX CC express proteins useful for diagnosing the presence of NDK and
XX CC related viruses and in vaccines against immunodeficiency diseases.
XX CC See also AAR09301-4.
XX
XX SQ Sequence 86 AA:
XX
XX Query Match 89.7%; Score 52; DB 11; Length 86;
XX Best Local Similarity 81.8%; Pred. No. 0.25;
XX Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YGRRKKRRQKK 11
XX |||||:|
XX Db 47 ygrrkkrrgrrk 57
XX
XX RESULT 3
XX AAM50263
XX ID AAM50263 standard; Protein; 11 AA.
XX
XX AC AAM50263;
XX
XX XX 20-JUL-1998 (first entry)
XX
XX DE HIV-1 tat protein.
XX
XX XX
XX KW Mouse; BH3 interacting domain death agonist; BID; BCL-2 family;
XX KW apoptosis; regulation; cell death; inflammation; cancer; arthritis;
XX KW autoimmune disease; viral infection; lymphoproliferative.
XX
XX OS Human immunodeficiency virus type 1.
XX
XX PN WO9809980-A1.
XX
XX PD 12-MAR-1998.
XX
XX PF 09-SEP-1997; 97WO-US15872.
XX
XX PR 09-SEP-1996; 96US-0706741.
XX
XX PA (UNIV ) UNIV WASHINGTON.
XX
XX PI Korsmeyer SJ;
XX PI WPI; 1998-193546/17.
XX
XX DR
XX XX
XX PD BH3 interacting domain death agonist polypeptide - used for treating
XX PD decreased apoptotic conditions resulting from inflammation etc.
XX
XX PF Example 8; Page 85; 118pp; English.

```

XX The present sequence represents the HIV-1 tat protein which is used in
CC an example of the present invention which describes a BH3 interacting
CC domain death agonist (BID) truncated protein. The BID protein, the
CC DNA encoding it or antisense sequences can be used for preventing or
CC treating a decreased apoptotic state of a cell. The decreased apoptotic
CC state that is treated results from a disease such as cancer, viral
CC infections, lymphoproliferative conditions, arthritis, inflammation and
CC autoimmune diseases. Antibodies against the BID protein can be used for
CC detecting a BID polypeptide in a cell or population of cell. The nucleic
CC acid sequence and the BID protein can also be used for treating
CC immunodeficiency disease (including AIDS), senescence, neurodegenerative
CC disease, ischemic and reperfusion cell death, infertility and
CC wound-healing. Primers derived from the nucleic acid encoding the BID
CC protein can be used for detecting/quantitating the protein and for
CC detecting alterations in the nucleic acid encoding the BID protein.
XX

SQ Sequence 11 AA;

Query Match 84.5%; Score 49; DB 19; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.12; Mismatches 0; Gaps 0;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRQKK 11

Db 1 YGRRKRRQRR 11

RESULT 4

AAV25075 standard; peptide: 11 AA.

AC AAV25075;

DT 24-AUG-1999 (first entry)

DE TAT transduction domain peptide motif.

XX Anti-pathogen: fusion protein; protein transduction domain; PMD; AZT;
KW Cytotoxic domain; suppressor; infection; medication; ddI; dC; dAT; 3TC;
KM FIC; DAPD; 1992089; CS92; acyclovir; ganciclovir; peniclovir; interferon;
KM apoptosis; virus; HIV; cytomegalovirus; CMV; herpes simplex virus; HSV-1;
KM hepatitis virus; Kaposi's sarcoma-associated herpes virus; KSHV;
KM herpes virus; yellow fever virus; flavivirus; rhinovirus; plasmoidal;
transduction efficiency; cytotoxin.

XX Unidentified.

OS Unidentified.

PN WO9929721-A1.

PD 17-JUN-1999.

PF 10-DEC-1998; 98WO-US26358.

PR 20-APR-1998; 98US-0082402.

PA (UNIV) UNIV WASHINGTON.

PI Dowdy SF;

DR WPI; 1999-394958/33.

PT New anti-pathogen systems, particularly for virus and plasmodium

PS Claim 65; Page 34; 123pp; English.

XX This invention describes a novel anti-pathogen system (APS) comprising a
CC fusion protein constructed from a covalently linked protein transduction
CC domain (PTD) and a cytotoxic domain. The APS can be used for suppressing
CC a pathogen infection in a mammal. The method may further comprise

CC administering a medicament e.g. AZT, ddI, ddC, d4T, 3TC, FIC, DAPD,
CC 1992089, CS92, acyclovir, ganciclovir, peniclovir or an interferon. The
CC APS can also be administered to a mammal in the presence of a pathogen to
CC induce apoptosis in a predetermined population of cells. The products can
CC be used for treating mammals suffering from or susceptible to a viral
CC infection or a disease associated with a virus, e.g. HIV, cytomegalovirus
CC (CMV), herpes simplex virus, e.g. type 1 (HSV-1) hepatitis virus, type C
CC (HCV), Kaposi's sarcoma-associated herpes virus (KSHV or human herpes
CC virus 8), yellow fever virus, flavivirus or rhinovirus, or suffering from
CC or susceptible to plasmoidal infection or a disease associated with a
CC plasmoidal infection, e.g. P. falciparum, P. vivax, P. ovale, or
CC P. malariae. The APS exhibits high transduction efficiency and
CC specifically kills or injures cells infected by one or more pathogens.
CC Formation of the cytotoxin is minimized or eliminated in uninfected cells
CC and in infected cells that keep the pathogen inactive. The APS can be
CC specifically tailored to kill or injure cells infected by one or more
CC pathogen strains. This sequence represents a TAT transduction domain
CC peptide motif which is used in the method of the invention.
XX

SQ Sequence 11 AA;

Query Match 84.5%; Score 49; DB 20; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.12; Mismatches 0; Gaps 0;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRQKK 11

Db 1 YGRRKRRQRR 11

RESULT 5

AAV05415 standard; peptide: 11 AA.

AC AAV05415;

DT 02-JUL-1999 (first entry)

DE Tat peptide.

XX BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
KM autoantibody producing cell; cancer; lymphoproliferative condition;
KW arthritis; autoimmune disease; therapy.

XX Unidentified.

OS Unidentified.

PN WO9916787-A1.

PD 08-APR-1999.

PF 22-SEP-1998; 98WO-US19765.

PR 07-OCT-1997; 97US-0946039.

PA 26-SEP-1997; 97US-0060133.

PA (UNIV) UNIV WASHINGTON.

PI Kormeyer SJ;

DR WPI; 1999-255058/21.

PT Bcl homology domain 3 polypeptide

PS Claim 7; Page 67; 104pp; English.

XX This sequence represents a Tat peptide.
CC The invention relates to a bcl homology domain 3 (BH3 domain),
CC derived from a proapoptotic member of the BCL-2 family. The
CC BH3 polypeptide can be used in a method for promoting apoptosis in a
CC target cell, especially where the cell is a cancer cell or a virus infected
CC cell or an autoantibody producing cell. The BH3 polypeptide can be used

CC in therapeutic compositions for treating disease including cancer, other
CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
CC diseases, which may result from the down regulation of cell death
CC regulation.

XX Sequence 11 AA;

Query Match 84.5%; Score 49; DB 20; Length 11;
Best Local Similarity 72.7%; Pred No. 0.12;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRRRRQKK 11
|||||
Db 1 ygrkrrrrrr 11

RESULT 6

AAB03932
ID AAB03932 standard; peptide; 11 AA.

XX AAB03932;

XX 26-FEB-2001 (first entry)

XX TAR protein transduction domain (internalisation moiety).

XX Modulating agent; beta-catenin; hair loss; hair growth; skin;

XX exfoliation; Alzheimer's disease; gene transcripion;

XX cell differentiation; hearing loss; inner ear; hyperacusis; tinnitus;

XX hair regeneration.

XX Human immunodeficiency virus (HIV).

XX WO200059939-A1.

XX 12-OCT-2000.

XX 04-APR-2000; 2000WO-US09174.

XX 05-APR-1999; 99US-0288373.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk CW, Byers S, Gour BJ;

XX WPI: 2000-679355/66.

XX Modulating agents for inhibiting degradation of cytoplasmic

XX beta-catenin, used for e.g. stimulating hair growth or reducing hair

XX loss, inhibiting development of Alzheimer's disease, comprise

XX internalization moiety and amino acid sequence

XX Claim 4; Page 46; 49pp; English.

XX Modulating agents for inhibiting degradation of cytoplasmic

XX beta-catenin are described. The modulating agent comprises an

XX internalisation moiety and one or more of an amino acid sequence

XX SYUS(PQ_4)GIS(PQ_4)G, or a peptide analogue or peptidomimetic of

XX the amino acid sequence. The modulating agents are useful for the

XX manufacture of a medicament for stimulating hair growth or reducing

XX hair loss, stimulating skin exfoliation, and inhibiting the

XX development of Alzheimer's disease. They may also be used to

XX increase the beta-catenin level in a cell, to stimulate activation

XX of gene transcription in a cell, and to stimulate cell

XX differentiation. They may further be used to ameliorate hearing loss

XX resulting from a variety of inner ear disorders, such as hyperacusis

XX and tinnitus, through regeneration of hair cells of the inner ear.

XX Sequence 11 AA;

XX Query Match, 84.5%; Score 49; DB 21; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.12;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRRRRQKK 11
|||||
Db 1 ygrkrrrrrr 11

RESULT 7

AAB03961
ID AAB03961 standard; Peptide; 11 AA.

XX AAB03961;

XX 26-FEB-2001 (first entry)

XX Minimal eleven amino acids present in PTAT.

XX Chimeric protein; fusion protein; FLICE like inhibitor protein;

XX FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;

XX tumour specific antigen; immune response; therapy; prophylaxis;

XX diagnosis; HIV; human immunodeficiency syndrome; AIDS;

XX acquired immune deficiency syndrome.

XX Human immunodeficiency virus.

XX WO200059935-A1.

XX 12-OCT-2000.

XX 05-APR-2000; 2000WO-US09002.

XX 05-APR-1999; 99US-0127867.

XX 06-APR-1999; 99US-0128021.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

XX (PATA/) PATA C.

XX (ALGE/) ALGECIRAS-SCHMINICH A.

XX Paya C, Algeciras-schminich A;

XX WPI: 2000-664988/64.

XX Fusion polypeptide useful for inhibiting ligand-induced apoptosis,

XX comprises portion of anti-apoptotic polypeptide linked to a transport

XX group

XX Disclosure; Page 30; 89pp; English.

XX A chimeric group or fusion peptide which comprises a portion of an

XX anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in

XX combination with a transport group is described. The transport group

XX is capable of transporting the chimeric group or fusion peptide

XX across the cell membrane. The anti-apoptotic polypeptide is FLICE-like

XX inhibitor protein (FLIP) which inhibits Fas and TNF mediated apoptosis

XX by inhibiting binding of Caspase-8 to the Fas receptor complex, thus

XX shutting off the downstream Fas signalling pathway. The chimeric group

XX and fusion peptide are useful for inhibiting ligand-induced apoptosis

XX by bringing them into contact with T cells. The chimeric group is

XX useful for expanding T cells in vitro e.g. T cells specific for

XX particular antigens such as tumour-specific antigen, for enhancing

XX immune response and to inhibit the apoptosis of chronically activated

XX T cells e.g. activated CD4+ T cells in HIV infected patients. The

XX chimeric group is also useful for therapeutic, prophylactic or

XX diagnosis of intracellular delivery of small molecules and

XX macromolecules such as anti-apoptotic polypeptides and nucleic

XX acids encoding such polypeptides. Two primers (AAs4297, AAs4298) were

XX used to amplify the FLIP cDNA for subcloning into the XhoI-NcoI

XX site of the pHA-TAT vector which contains the N-terminal protein

XX transduction domain from the human immunodeficiency virus tat

XX protein. Tat is a preferred transport moiety.

XX Sequence 11 AA;

XX Query Match, 84.5%; Score 49; DB 21; Length 11;

Query Match 84.5%; Score 49; DB 21; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.12;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRQKKK 11
DB 1 YGRRKRRQRR 11

RESULT 8

AAB27088
ID AAB27088 standard; Peptide; 11 AA.

XX AAB27088;

DT 15-FEB-2001 (first entry)

DE Beta-catenin derived internalisation moiety SEQ ID NO: 75.

XX Beta-catenin; cadherin-mediated intercellular adhesion;

KW cell differentiation; modulating agent; hair loss; skin exfoliation;
XX internalisation moiety; flanking sequence; transcription; hearing loss.

OS Human immunodeficiency virus.

XX WO200053632-A1.

XX 14-SEP-2000.

XX 07-MAR-2000; 2000WO-CA00222.

XX 09-MAR-1999; 99US-0265107.

PA (UYMC-) UNIV MCGILL.

PI Blaschuk OM, Gour BJ;

DR WPI; 2000-594308/56.

PT Stimulating beta-catenin mediated gene expression, cellular
PT differentiation and hair growth, involves contacting cells with
PT modulating agent capable of inhibiting interaction between alpha and
PT beta catenin -

PS Disclosure: Page 19; 77pp; English.

CC The present invention is concerned with methods of modulating the amount
CC of free beta-catenin in the cell, and methods of stimulating the
CC expression of genes involved in cellular differentiation, the
CC transcription of which is under the control of beta-catenin. The
CC peptides given in AAB27053-B27088, AAB27284-B27300 and AAB27330-B27351
CC can be used as modulating agents which interrupt the interaction between
CC alpha and beta catenin, causing increased levels of the latter and
CC stimulating the activation of beta-catenin mediated transcription. This
CC can be used to stimulate cell differentiation, which can then be used to
CC promote hair growth and skin exfoliation. This latter can particularly
CC be useful in the improvement of photodamaged skin and to minimise wrinkles.
CC The modulating peptide can also be used to reduce hearing loss resulting
CC from inner ear disorders such as hyperacusis and tinnitus.

XX Sequence 11 AA;

Query Match

Best Local Similarity 84.5%; Score 49; DB 21; Length 11;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRQKKK 11
DB 1 YGRRKRRQRR 11

RESULT 9

AAB35698
ID AAB35698 standard; Peptide; 11 AA.

XX AAB35698;

DT 16-FEB-2001 (first entry)

DE Peptide associated with modified beta-catenin expression #31.

XX Beta-catenin; cell differentiation; hair growth;

KW cancer; Alzheimer's disease.

XX Human immunodeficiency virus type 1.

XX WO200063246-A2.

XX 26-OCT-2000.

XX 21-APR-2000; 2000WO-US10753.

XX 21-APR-1999; 99US-0296089.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuk OM, Byers S, Gour BJ;

DR WPI; 2000-679589/66.

PT Use of modulating agent comprising internalization moiety and a
PT peptide, for modulating beta-catenin mediated gene transcription and
PT cell differentiation, for treating cancer, and for inhibiting
PT Alzheimer's disease -

PS Claim 6; Page 26; 47pp; English.

CC The present invention relates to a method for modulating beta-catenin
CC mediated gene transcription in a cell. The method involves contacting
CC a cell with a modulating agent comprising an internalization moiety
CC and a peptide comprising a sequence IXXLL or peptide analogue of IXXLL.
CC The method is useful for modulating beta-catenin mediated gene
CC transcription, cell differentiation, hair growth, and retinoic acid
CC activity, for treating cancer, and for inhibiting the development of
CC Alzheimer's disease.

XX Sequence 11 AA;

Query Match 84.5%; Score 49; DB 21; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.12;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRQKKK 11
DB 1 YGRRKRRQRR 11

RESULT 10

AAB29413
ID AAB29413 standard; peptide; 11 AA.

XX AAB29413;

DT 09-FEB-2001 (first entry)

DE HIV TAF transduction domain, SEQ ID NO:2.

KW Protein transduction domain; fusion molecule; therapeutic agent;
KW drug targeting; drug discovery; cell transduction; bioavailability;
KW vaccine; nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy;
KW seizure; compulsive behaviour; meningitis; encephalitis; ischaemia;

KW spongiform encephalopathy; dyslexia; age-related memory loss;
 XX Lou Gehrig's disease; viral infection; HIV; bacterial infection
 XX
 OS Human immunodeficiency virus.
 PN WO200062067-A1.
 XX
 PD 19-OCT-2000.
 XX
 PE 28-FEB-2000; 2000MO-US05097.
 XX
 PR 28-FEB-1999; 99US-0122757.
 PR 29-AUG-1999; 99US-0151291.
 XX
 XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PI Dowdy SF;
 XX
 DR WPI; 2000-647439/62.
 XX
 PT Fusion molecules comprising protein transduction domains and
 PT therapeutic agents, useful for treating e.g. Alzheimer's and
 PT Parkinson's diseases, dementia and epilepsy -
 XX
 PS Disclosure; Page 50; 191pp; English.

```

OY 1 YGRKKRRÖKK 11
    |||||:::
Db 1 YGRKKrrrrr 11

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RESULT , 11
AAB09907
ID      AAB09907 standard; peptide; 11 AA.
XX

```

AC	AAB09907;
XX	
DT	06-NOV-2000 (first entry)

AA Targeting signal; MUC-1; immunosuppression; autoimmune disorder.
 KW immune disorder; inflammatory disorder.

OS Human immunodeficiency virus.

PN WO200034468-A2.

PD 15-JUN-2000.

PF 09-DEC-1999; 99WO-US29016.

PR 11-DEC-1998; 98US-0111973.

PA (BIOM-) BIOMIRA INC.

PI Agrawal B, Longenecker BM

DR WPI; 2000-423418/36.

PT Use of agent capable of intracellularly inhibiting mucin MUC-1 for
PT inducing T-cell based immunosuppression and for treating autoimmune
PT disorders, transplant rejection and inflammatory disorders -
XX
PS Disclosure; Page 15; Sipp; English.

SQ Sequence 11 AA

Query Match	84.58;	Score 49;	DB 21;	Length 11;
Best Local Similarity	72.78;	Pred. No. 0.12;		
Matches	8;	Conservative	0;	Indels 0;
		Mismatches	0;	Gaps 0;

QY	1	YGRKKRRÖKK	11
		:::	
Db	1	YGRKKrrrrr	11

RESULT	12
AAV93542	
ID	AAV93542 standard; Peptide; 11 AA

AC AAY93542

DT 25-SEP-2000 (first entry)

DE Amino acid sequence of a synthetic protein transduction domain
XX
KW Protein transduction system; protein transduction domain;
KW cytotoxic domain; pathogen infection; retroviral infection;
KW plasmoidal infection; cancer; prostate cancer.

XX	Synthetic.
OS	
XX	WO200034308-A2.
PN	
XX	15-JUN-2000.
PD	
XX	10-DEC-1999; 99WO-US29289.
PF	
XX	10-DEC-1998; 98US-0111701.
PR	(UNIW) UNIV WASHINGTON.
PA	
XX	Dowdy SF;
PI	
DR	WPI: 2000-431269/37.
XX	
PT	Protein transduction system for treating cancer and pathogenic
XX	infections has a fusion protein comprising a protein transduction
CC	domain covalently linked to a cytotoxic domain
PS	
XX	Example 10; Page 71; 127pp; English.
CC	AAY93542-51 represent synthetic protein transduction domains, which
CC	are used in the protein transduction system of the invention. The
CC	specification describes a protein transduction system, which comprises
CC	a fusion protein. This fusion protein has a covalently linked protein
CC	transduction domain and cytotoxic domain. The system is useful for
CC	treating pathogen infection in mammals, infections such as those
CC	caused by CMV, HSV-1, HCV, KSHV, yellow fever virus, flavivirus or
CC	rhinovirus, retroviral infections such as HIV-1, HIV-2, HTLV-3 and/or
CC	LAV, plasmodial infections associated with P.faciaparum, P.vivax,
CC	P.ovale, P.malariae. It is also useful for treating cancer, especially
SO	prostate cancer.
Sequence	11 AA:
Query Match	84.5%; Score 49; DB 21; Length 11;
Best Local Similarity	72.7%; Pred. No. 0.12;
Matches	8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY	1 YGRRKKRKKK 11 N ::: DB 1 ygrkkrrqrrr 11
RESULT 13	
ID	AAY71015 standard; peptide: 11 AA. AAY71015
AC	AAY71015;
XX	
DT	29-AUG-2000 (first entry)
XX	
DE	Human immunodeficiency virus TAT peptide.
KM	Phospholamban; PLB; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; HIV;
KW	TAT protein; penetratin; transport peptide; cardiomyocyte inhibitor;
KM	cargo peptide; contractilin; cardiac contractility; cardiac treatment;
XX	cardiac disease; heart failure; myocardial dysfunction.
OS	
XX	Human immunodeficiency virus.
XX	
PN	WO200025804-A2.
PD	
XX	11-MAY-2000.
XX	
PE	02-NOV-1999; 99WO-US25692.
XX	
PR	02-NOV-1998; 98US-0106718.
PR	27-JUL-1999; 99US-0145883.

(REGC) UNIV CALIFORNIA.
 Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 Scott C, Wang Y, Silverman GJ;
 WPI: 2000-365393/31.
 Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 comprises enhancing cardiac contractility by inhibiting interaction
 between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 triphosphatase -
 Example 5; Page 54; 56pp; English.
 The patent discloses a method for the treatment of heart failure, using
 small peptide complexes and recombinant proteins, that induces
 phospholamban (PLB) deficiency and inhibits the interaction between PLB
 and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes
 CC The peptide complex comprises of transport peptide like penetratin and
 cargo peptide selected from mutant PLB, native PLB or antibody against
 PLB protein (contractilin). Penetratin-PLB peptide functions as a
 dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardia
 contractility and reduces blood pressure. This method is useful for the
 treatment of cardiac disease e.g. heart failure and myocardial
 dysfunction. The present sequence is the amino terminal, 11-amino acid
 CC protein transduction domain of the denuatured human immunodeficiency
 virus (HIV) Tat protein. It belongs to the penetratin class of peptides
 CC with translocating properties having the ability to carry hydrophilic
 compounds across the plasma membrane. It is used in the construction of
 recombinant PLB peptides (e.g., TAT-PLB).
 Sequence 11 AA;

```

Query Match: 84.5%; Score 49; DB 21; Length 11;
Best Local Similarity 72.7%;
Pred. No. 0.12;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0.

QY      1 YGRKKRRQRRK 11
      |||||
Db      1 YGRKKRRQRR 11

RESULT 14
AAU09332
AAU09332 standard; Peptide: 11 AA.
XX
AC      AAU09332;
XX
DT      15-JAN-2002 (first entry)
XX
DE      Human immunodeficiency virus (HIV) tat partial peptide sequence.
XX
KW      Human: fibroblast growth factor-like; RGF-L; HIV tat protein;
KW      protein transduction domain; PDT; human immunodeficiency virus.
XX
OS      Human immunodeficiency virus type 1.
XX
WO200168854-A2.
XX
PN      20-SEP-2001.
XX
PD      13-MAR-2001; 2001WO-US08013.
XX
PF      13-MAR-2000; 2000US-188786P.
XX
PR      (AMGE-) AMGEN INC.
XX
PA      Jing S, Bass MB;
XX
PI      WPI, 2001-596910/67.
XX
DR      New fibroblast growth factor-like polypeptide and polynucleotide for
XX      PT

```

PT diagnosis, prevention and treatment of diseases, disorders or
PT conditions involving the central nervous system, teeth, heart, liver or
PT adipose tissue -
PS Disclosure; Page 62; 116pp; English.
XX
CC The present invention relates to new isolated fibroblast growth
CC factor-like (FGF-L) nucleic acid molecules and polypeptides. The FGF-L
CC polypeptide is useful for determining whether a compound inhibits FGF-L
CC polypeptide, and also for identifying a compound that binds to the
CC polypeptide. The FGF-L polypeptides of the invention are useful for
CC treating, preventing or ameliorating a medical condition or an FGF-L
CC polypeptide-related disease, condition or disorder such as wound healing
CC disorders, ulcers, gut disorders, lung disorders, liver disorders such as
CC hepatitis and diabetes. The invention is also useful for diagnosing a
CC pathological condition or susceptibility to a pathological condition in
CC a subject and is useful for modulating levels of FGF-L in an animal.
CC Other uses are detecting or quantifying the amount of FGF-L polypeptide
CC and for identifying or developing novel agonists and antagonists of the
CC FGF-L polypeptide signaling pathway which are useful for treating one
CC or more diseases or disorders, and also as an immunogen for producing
CC antibodies for in vivo imaging. The present sequence represents an 11
CC amino acid sequence from the human immunodeficiency virus (HIV) tat
CC protein that is termed the protein transduction domain or TAT PDT.
XX
SQ Sequence 11 AA:
OY 1 YGRKKRRQKK 11
DB 1 YGRKKRRQRR 11
RESULTS 15
AAU09812
ID AAU09812 standard; Protein; 11 AA.
XX
AC AAU09812;
XX
DT 27-FEB-2002 (first entry)
XX
DE HIV-1 tat protein transduction domain (TAT PDT).
XX
KW fibroblast growth factor receptor-like protein; FGFR-L; anorectic;
KW haemostatic; osteopathic; cytostatic; nephrotropic; antidiabetic;
KW immunomodulator; antiinflammatory; haematopoietic disorder; osteoporosis;
KW osteogenesis imperfecta; Paget's disease; periodontal disease; cancer;
KW hypercalcaemia; acute glomerulonephritis; chronic glomerulonephritis;
KW diabetes; obesity; cachexia; transgenic animal; gene therapy.
XX
KW human immunodeficiency virus; HIV-1; tat protein.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200170977-A2.
XX
PD 27-SEP-2001.
XX
PF 22-MAR-2001; 2001WO-US09073.
XX
PR 22-MAR-2000; 2000US-191379P.
XX
PA (AMGE-) AMGEN INC.
PA (SARI/) SARIS C M.
PA (MUSX/) MU S X.
PA (XIAM/) XIA M.
PA (BOON/) BOONE T C.
PA (COVE/) COVEY T.
XX
PI Saris CM, Mu SX, Xia M, Boone TC, Covey T;

XX
DR WPI: 2001-626128/72.
XX
PT Novel nucleic acid encoding fibroblast growth factor receptor-like
PT polypeptides, useful for treating hematopoietic disorder, osteoporosis,
PT Paget's disease, glomerulonephritis, cancer, diabetes, obesity and
PT cachexia -
PS Disclosure; Page 59; 163pp; English.
XX
XX The invention relates to a novel isolated fibroblast growth factor
XX receptor-like (FGFR-L) polypeptide (I). (I) and the nucleic acid (II)
XX encoding (I) are useful for treating, preventing or ameliorating
XX a medical condition including hematopoietic disorder, osteoporosis,
XX osteogenesis imperfecta, Paget's disease, periodontal disease,
XX hypercalcaemia, acute glomerulonephritis, chronic glomerulonephritis,
XX cancer, diabetes, obesity and cachexia. (I) is also useful for
XX identifying a compound which binds to FGFR-L polypeptide, by contacting
XX (I) with a compound, determining the extent of binding of the FGFR-L
XX polypeptide to the compound, and determining the activity of the
XX polypeptide when bound to the compound. (II) is useful for modulating
XX levels of a polypeptide in an animal. A transgenic animal comprising (I)
XX is useful for determining whether a compound inhibits FGFR-L polypeptide
XX activity or FGFR-L polypeptide production, by exposing the transgenic
XX animal to the compound and measuring FGFR-L polypeptide or production in
XX the mammal. (II) is useful for mapping the locations of FGFR-L gene and
XX related genes on chromosomes, as hybridisation probes in diagnostic
XX assays to test for the presence of an FGFR-L nucleic acid molecule in
XX mammalian tissue or bodily fluid samples, in gene therapy, and as tools
XX for isolating corresponding FGFR-L polypeptide genes. (I) is useful as
XX immunogen, and for cloning FGFR-L polypeptide ligands using an
XX expression cloning strategy. The present sequence represents the
XX amino acid sequence of human immunodeficiency virus (HIV-1) tat protein
XX transduction domain (TAT PDT) as described in the invention.
SQ Sequence 11 AA:

Query Match 84.5%; Score 49; DB 22; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.12;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 YGRKKRRQKK 11
DB 1 YGRKKRRQRR 11

Search completed: July 15, 2002, 12:57:59
Job time: 415 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:59:19 ; Search time 75.67 Seconds

(without alignments)
3.551 Million cell updates/sec

Title: US-09-712-819A-8

Perfect score: 58

Sequence: 1 YGKRRKQKK 11

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	49	84.5	11	2	US-08-706-741B-54
2	49	84.5	11	2	US-08-924-695A-54
3	49	84.5	11	4	US-09-208-966-2
4	49	84.5	11	4	US-09-296-089-37
5	49	84.5	12	1	US-08-450-257-47
6	49	84.5	12	1	US-08-450-246-47
7	49	84.5	12	1	US-08-450-098-47
8	49	84.5	12	1	US-08-451-233-47
9	49	84.5	12	1	US-08-450-236-47
10	49	84.5	12	2	US-08-733-505A-50
11	49	84.5	12	4	US-08-235-403-47
12	49	84.5	14	5	PCR-US95-06077-4
13	49	84.5	14	5	PCR-US95-06077-10
14	49	84.5	14	5	PCR-US95-06077-11
15	49	84.5	14	5	PCR-US95-06077-12
16	49	84.5	15	1	US-08-450-257-5
17	49	84.5	15	1	US-08-450-257-6
18	49	84.5	15	1	US-08-450-246-5
19	49	84.5	15	1	US-08-450-246-6
20	49	84.5	15	1	US-08-450-098-5
21	49	84.5	15	1	US-08-450-098-6
22	49	84.5	15	1	US-08-451-233-5
23	49	84.5	15	1	US-08-451-233-6
24	49	84.5	15	1	US-08-450-236-5
25	49	84.5	15	1	US-08-450-236-6
26	49	84.5	15	4	US-08-235-403-5
27	49	84.5	15	4	US-08-235-403-6

28	49	84.5	17	2	US-08-902-623-7	Sequence 7, Appl1
29	49	84.5	18	5	PCR-US95-06077-3	Sequence 3, Appl1
30	49	84.5	21	1	US-08-450-257-50	Sequence 50, Appl1
31	49	84.5	21	1	US-08-450-246-50	Sequence 50, Appl1
32	49	84.5	21	1	US-08-450-098-50	Sequence 50, Appl1
33	49	84.5	21	1	US-08-451-233-50	Sequence 50, Appl1
34	49	84.5	21	1	US-08-450-236-50	Sequence 50, Appl1
35	49	84.5	21	4	US-08-235-403-50	Sequence 50, Appl1
36	49	84.5	22	1	US-08-450-257-3	Sequence 3, Appl1
37	49	84.5	22	1	US-08-450-246-3	Sequence 3, Appl1
38	49	84.5	22	1	US-08-450-098-3	Sequence 3, Appl1
39	49	84.5	22	1	US-08-451-233-3	Sequence 3, Appl1
40	49	84.5	22	1	US-08-450-236-3	Sequence 3, Appl1
41	49	84.5	22	4	US-08-235-403-3	Sequence 3, Appl1
42	49	84.5	24	1	US-08-450-257-4	Sequence 4, Appl1
43	49	84.5	24	1	US-08-450-246-4	Sequence 4, Appl1
44	49	84.5	24	1	US-08-450-098-4	Sequence 4, Appl1
45	49	84.5	24	1	US-08-451-233-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-706-741B-54
; Sequence 54, Application US/08706741B
; Patent No. 5955593
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,741B
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO.: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-706-741B-54

Query Match 84.5%; Score 49; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.067;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRKQKK 11
DB 1 YGKRRKQRR 11

RESULT 2
US-08-924-695A-54
; Sequence 54, Application US/08924695A
; Patent No. 5998583
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/924,695A
; FILING DATE: 09-SEP-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 9711798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-924-695A-54

Query Match 84.5%; Score 49; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.067;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRQKK 11
DB 1 YGRRKRQRR 11

RESULT 3
US-09-208-966-2
; Sequence 2, Application US/09208966
; Patent No. 6221355
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/208,966
; EARLIER FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: 60/069,012
; EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-208-966-2

Query Match 84.5%; Score 49; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.067;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRQKK 11
DB 1 YGRRKRQRR 11

RESULT 4
US-09-296-089-37
; Sequence 37, Application US/09296089
; Patent No. 6303576
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: 100086,411
; CURRENT APPLICATION NUMBER: US/09/296,089
; FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-296-089-37

Query Match 84.5%; Score 49; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.067;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRQKK 11
DB 1 YGRRKRQRR 11

RESULT 5
US-08-450-257-47
; Sequence 47, Application US/08450257
; Patent No. 5652122
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPIŃSKY, R. B.
; TITLE OF INVENTION: TAX-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,257
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992

APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-257-47

Query Match 84.5% Score 49; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKKRRQKKK 11
|||||
Db 1 YGKKRRQRRR 11

RESULT 6
US-08-450-246-47
Sequence 47, Application US/08450246
Patent No. 5670617
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPIISKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,246
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833

FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-246-47

Query Match 84.5% Score 49; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKKRRQKKK 11
|||||
Db 1 YGKKRRQRRR 11

RESULT 7
US-08-450-098-47
Sequence 47, Application US/08450098
Patent No. 5674980
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPIISKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989

APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-098-47

Query Match 84.5%; Score 49; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKRRRQKK 11
DB 1 YGKRRRQRR 11

RESULT 8
US-08-451-233-47

; Sequence 47, Application US/08451233

; Patent No. 5747641

; GENERAL INFORMATION:

; APPLICANT: FRANKEL, Alan

; APPLICANT: PABO, Carl

; APPLICANT: BARSQUM, James G.

; APPLICANT: FAWELL, Stephen E.

; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FISH & NEAVE

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/451,233

; FILING DATE: 25-MAY-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/235,403

; FILING DATE: 28-APR-1994

; APPLICATION NUMBER: US 07/934,375

; FILING DATE: 21-AUG-1992

; APPLICATION NUMBER: US 07/098,766

; FILING DATE: 28-JUL-1993

; APPLICATION NUMBER: PCT/US93/07833

; FILING DATE: 19-AUG-1993

; APPLICATION NUMBER: US 07/454,450

; FILING DATE: 21-DEC-1989

; APPLICATION NUMBER: US 07/636,662

; FILING DATE: 02-JAN-1991

; APPLICATION NUMBER: US 08/158,015

FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-451-233-47

Query Match 84.5%; Score 49; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKRRRQKK 11
DB 1 YGKRRRQRR 11

RESULT 9
US-08-450-236-47

; Sequence 47, Application US/08450236

; Patent No. 5804604

; GENERAL INFORMATION:

; APPLICANT: FRANKEL, Alan

; APPLICANT: PABO, Carl

; APPLICANT: BARSQUM, James G.

; APPLICANT: FAWELL, Stephen E.

; APPLICANT: PEPIISKY, R. B.

; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FISH & NEAVE

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,236

; FILING DATE: 25-MAY-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/235,403

; FILING DATE: 28-APR-1994

; APPLICATION NUMBER: US 07/934,375

; FILING DATE: 21-AUG-1992

; APPLICATION NUMBER: US 07/098,766

; FILING DATE: 28-JUL-1993

; APPLICATION NUMBER: PCT/US93/07833

; FILING DATE: 19-AUG-1993

; APPLICATION NUMBER: US 07/454,450

; FILING DATE: 21-DEC-1989

; APPLICATION NUMBER: US 07/636,662

; FILING DATE: 02-JAN-1991

; APPLICATION NUMBER: US 08/158,015

; FILING DATE: 24-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-236-47

Query Match 84.5%; Score 49; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRRRRQKK 11
DB 1 YGRRRRRQRR 11

RESULT 10
US-08-733-505A-50
Sequence 50, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-50

Query Match 84.5%; Score 49; DB 2; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRRRRQKK 11
DB 1 YGRRRRRQRR 11

DB 1 YGRRRRRQRR 11

RESULT 11
US-08-235-403-47
Sequence 47, Application US/08235403
Patent No. 6316003
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOOM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,403
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JR., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-235-403-47

Query Match 84.5%; Score 49; DB 4; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRRRRQKK 11
DB 1 YGRRRRRQRR 11

RESULT 12
PCT-US95-06077-4

Sequence 4, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Interellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR144PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-06077-4

Query Match 84.5%; Score 49; DB 5; Length 14;
Best Local Similarity 72.7%; Pred. No. 0.081;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKKRRQKKK 11
DB 2 YGKKRRQRRR 12

RESULT 13
PCT-US95-06077-10
Sequence 10, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Interellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR144PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-06077-10

Query Match 84.5%; Score 49; DB 5; Length 14;
Best Local Similarity 72.7%; Pred. No. 0.081;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKKRRQKKK 11
DB 2 YGKKRRQRRR 12

RESULT 14
PCT-US95-06077-11
Sequence 11, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Interellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR144PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid

TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-06077-11

Query Match 84.5%; Score 49; DB 5; Length 14;
Best Local Similarity 72.7%; Pred. No. 0.081;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRRRRROKKK 11
|||||
Db 2 YGRRRRROKKK 12

RESULT 15
PCT-US95-06077-12
Sequence 12, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Intercellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IRI44PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-06077-12

Query Match 84.5%; Score 49; DB 5; Length 14;
Best Local Similarity 72.7%; Pred. No. 0.081;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRRRRROKKK 11
|||||
Db 2 YGRRRRROKKK 12

Search completed: July 15, 2002, 12:59:20
Job time: 391 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:01:03 ; Search time 95.45 Seconds
(without alignments)
29.194 Million cell updates/sec

Title: US-09-712-819A-9

Perfect score: 144
Sequence: 1 YERRRRRRRRSGSGTDFTLTITSSLOAED 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	87	60.4	92	2 S37533	Ig kappa chain V r
2	87	60.4	92	2 S37530	Ig kappa chain V r
3	87	60.4	92	2 S37529	Ig kappa chain V r
4	87	60.4	92	2 S37535	Ig kappa chain V r
5	87	60.4	92	2 S37531	Ig kappa chain V r
6	87	60.4	92	2 S37534	Ig kappa chain V r
7	87	60.4	92	2 S37532	Ig kappa chain V r
8	87	60.4	101	2 PH0869	Ig kappa chain V r
9	87	60.4	102	2 B34153	Ig kappa chain V r
10	87	60.4	106	2 A49138	Ig kappa chain V r
11	87	60.4	113	2 S30523	Ig kappa chain V r
12	87	60.4	113	2 S30520	Ig kappa chain V r
13	87	60.4	113	2 S34003	Ig kappa chain V r
14	87	60.4	113	2 S34002	Ig kappa chain V r
15	87	60.4	114	1 K4HUN	Ig kappa chain V r
16	87	60.4	114	2 S44116	Ig kappa chain V r
17	87	60.4	120	2 S51147	Ig kappa chain V r
18	87	60.4	121	1 K4HU	Ig kappa chain V r
19	87	60.4	124	2 S40364	Ig kappa chain V r
20	87	60.4	133	1 K4HUI	Ig kappa chain V r
21	87	60.4	134	1 K4HUI	Ig kappa chain V r
22	87	60.4	134	2 S49531	Ig kappa chain V r
23	84	58.3	79	2 S24215	Ig kappa chain V r
24	84	58.3	81	2 PH1048	Ig kappa chain V r
25	84	58.3	97	2 A42575	Ig kappa chain V r
26	84	58.3	101	2 S26337	Ig kappa chain V r
27	84	58.3	101	2 PH1046	Ig kappa chain V r
28	84	58.3	102	2 A34153	Ig kappa chain V r
29	84	58.3	103	2 PH1050	Ig kappa chain V r

30	84	58.3	103	2 PH1051	Ig light chain V r
31	84	58.3	103	2 PH1052	Ig light chain V r
32	84	58.3	103	2 PH1054	Ig light chain V r
33	84	58.3	103	2 PH1047	Ig light chain V r
34	84	58.3	104	2 PH1053	Ig light chain V r
35	84	58.3	104	2 PH1101	Ig light chain V r
36	84	58.3	104	2 PH1102	Ig light chain V r
37	84	58.3	104	2 PH1103	Ig light chain V r
38	84	58.3	104	2 PH1104	Ig light chain V r
39	84	58.3	104	2 C30534	Ig kappa chain V r
40	84	58.3	105	2 A30534	Ig kappa chain V r
41	84	58.3	107	2 B30535	Ig kappa chain V r
42	84	58.3	107	2 G30535	Ig kappa chain V r
43	84	58.3	107	2 D30535	Ig kappa chain V r
44	84	58.3	107	2 F30535	Ig kappa chain V r
45	84	58.3	107	2 S36268	Ig lambda chain V r

ALIGNMENTS

RESULT 1
S37533
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37533
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral bl
A:Reference number: S37501
A:Accession: S37533
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26627; NID:9405708; PIDN:CAA81380.1; PID:9405709
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGGDTFTLTITSSLOAED 29
DB 49 SSGGDTFTLTITSSLOAED 66

RESULT 2
S37530
Ig kappa chain V region (V-kappa 4) - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral bl
A:Reference number: S37501
A:Accession: S37530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26630; NID:9405702; PIDN:CAA81383.1; PID:9405703
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGGDTFTLTITSSLOAED 29

Db 49 SSGGDFLTITSSLOAED 66
|||||

RESULT 3

S37529
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37529
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226631; NID:9405700; PIDN:CAA81384.1; PID:9405701
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 SSGGDFLTITSSLOAED 29
|||||

RESULT 4

S37535
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37535
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226625; NID:9405712; PIDN:CAA81378.1; PID:9405713
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 SSGGDFLTITSSLOAED 29
|||||

RESULT 5

S37531
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37531
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37531
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226629; NID:9405704; PIDN:CAA81382.1; PID:9405705
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 SSGGDFLTITSSLOAED 29
|||||

RESULT 6

S37534
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37534
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226626; NID:9405710; PIDN:CAA81379.1; PID:9405711
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 SSGGDFLTITSSLOAED 29
|||||

RESULT 7

S37532
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37532
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226628; NID:9405706; PIDN:CAA81381.1; PID:9405707
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 SSGGDFLTITSSLOAED 29
|||||

RESULT 8

PH0869

Ig kappa chain V region (anti-DNA, H2F) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0869
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A:Reference number: PH0862; MUID:92078875
A:Accession: PH0869
A:Molecule type: DNA
A:Residues: 1-101 <MAN>
A>Note: residues 28-33 were obtained from Figure 4
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-96/Domain: immunoglobulin homology <IMM>
F:24-40/Region: complementarity-determining 1
F:41-55/Region: framework 2
F:56-62/Region: complementarity-determining 2
F:63-94/Region: framework 3
F:95-101/Region: complementarity-determining 3

Query Match 60.4%; Score 87; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGGTDFLTITSSLOAED 29
DB 71 SSGGTDFLTITSSLOAED 88

RESULT 9
B34153
Ig kappa chain V-IV region (Fue) - human
C:Species: Homo sapiens (man)
C>Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jan-2000
C:Accession: B34153
R:Milnesco, E.; Avadi, H.; Congy, N.; Gendron, M.C.; Roy, J.P.; Heyermann, H.; Frangione
J. Biol. Chem. 264, 21481-21485, 1989
A:Title: Multiple mutations in the variable region of the kappa light chains of three mc
A:Reference number: A34153; MUID:90094313
A:Accession: B34153
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-102 <MIH>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 87; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGGTDFLTITSSLOAED 29
DB 71 SSGGTDFLTITSSLOAED 88

RESULT 10
A49138
IgA kappa rheumatoid factor variable - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49138
R:Gause, A.; Kuppers, R.; Mierau, R.
Clin. Exp. Immunol. 88, 430-434, 1992
A:Title: A somatically mutated V kappa IV gene encoding a human rheumatoid factor light
A:Reference number: A49138; MUID:92298890
A:Accession: A49138
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-106 <GAD>
A:Cross-references: GB:S37926; NID:9298207; PID:AAE22366.1; PID:9298208
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:106633, NCBI:P:106637)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:20-99/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 87; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGGTDFLTITSSLOAED 29
DB 74 SSGGTDFLTITSSLOAED 91

RESULT 11
S30523
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30523
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30523
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z18329
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 87; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGGTDFLTITSSLOAED 29
DB 71 SSGGTDFLTITSSLOAED 88

RESULT 12
S30520
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30520
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30520
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z18325
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 87; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGGTDFLTITSSLOAED 29
DB 71 SSGGTDFLTITSSLOAED 88

RESULT 13

S34003
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34003
R:Marlette, X.; Tsaplis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281
A:Accession: S34003
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:16-96/Domain: Immunoglobulin homology <IMM>

Query Match

60.4%; Score 87; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGTDFTLTISLQAE 29
DB 71 SGGTDFTLTISLQAE 88

RESULT 14

S34002
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34002; S30522
R:Marlette, X.; Tsaplis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281
A:Accession: S34002
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
C:Cross-references: EMBL:218328
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:16-96/Domain: Immunoglobulin homology <IMM>

Query Match

60.4%; Score 87; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGTDFTLTISLQAE 29
DB 71 SGGTDFTLTISLQAE 88

RESULT 15

K4HULN
Ig kappa chain V-IV region (Len) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
C:Accession: A01903; F61458
R:Schneider, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975
A:Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette der Subgruppe IV
A:Reference number: A01903; MUID:76004342
A:Accession: A01903
A:Molecule type: protein
A:Residues: 1-114 <SCH>
A:Note: this is the first completely sequenced V region of a new kappa chain subgroup.
A:Note: the C' region of this chain has the Inv (3) marker

R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-a
A:Reference number: A61458; MUID:90039128
A:Accession: F61458
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRQ>

C:Comment: This is a Bence Jones protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: Immunoglobulin homology <IMM>
F:23-94/Disulfide bonds: #status predicted

Query Match

60.4%; Score 87; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGTDFTLTISLQAE 29
DB 71 SGGTDFTLTISLQAE 88

Search completed: July 15, 2002, 13:01:03
Job time: 469 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:23:34 ; Search time 44.9 Seconds
(without alignments)
25.008 Million cell updates/sec

Title: US-09-712-819A-9
Perfect score: 144
Sequence: 1 YERKKRRQRRRSGTDFLTITSLQAED 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	60.4	114	KVA4_HUMAN	P01625 homo sapien
2	87	60.4	121	KVA0_HUMAN	P06312 homo sapien
3	87	60.4	133	KVAB_HUMAN	P06313 homo sapien
4	87	60.4	134	KVAC_HUMAN	P06314 homo sapien
5	82	56.9	108	KV1H_HUMAN	P01600 homo sapien
6	82	56.9	116	KV3J_HUMAN	P04434 homo sapien
7	82	56.9	117	KV1I_HUMAN	P01601 homo sapien
8	82	56.9	129	KV1M_HUMAN	P04431 homo sapien
9	80	55.6	109	KV3F_HUMAN	P01632 homo sapien
10	80	55.6	114	KV1A_MOUSE	P01633 mus musculu
11	80	55.6	149	KV5A_MOUSE	P01633 mus musculu
12	79	54.9	108	KV1O_HUMAN	P01609 homo sapien
13	79	54.9	115	KV3I_HUMAN	P04433 homo sapien
14	78	54.2	108	KV1M_HUMAN	P01605 homo sapien
15	78	54.2	108	KV1S_HUMAN	P01611 homo sapien
16	78	54.2	108	KV1Y_HUMAN	P01611 homo sapien
17	78	54.2	136	KV5B_MOUSE	P01634 mus musculu
18	76	52.8	108	KV1C_HUMAN	P01595 homo sapien
19	76	52.8	108	KV1F_HUMAN	P04430 homo sapien
20	75	52.1	108	KV1E_HUMAN	P01598 homo sapien
21	75	52.1	108	KV1G_HUMAN	P01599 homo sapien
22	75	52.1	108	KV1O_HUMAN	P01607 homo sapien
23	75	52.1	108	KV1P_HUMAN	P01608 homo sapien
24	75	52.1	108	KV1R_HUMAN	P01610 homo sapien
25	75	52.1	117	KV1J_HUMAN	P01602 homo sapien
26	75	52.1	129	KV3H_HUMAN	P04207 homo sapien
27	74	51.4	107	KV1D_HUMAN	P01596 homo sapien
28	74	51.4	109	KV3D_HUMAN	P01622 homo sapien
29	74	51.4	109	KV3E_HUMAN	P01623 homo sapien
30	74	51.4	109	KV3G_HUMAN	P04206 homo sapien
31	74	51.4	129	KV3L_HUMAN	P18135 homo sapien
32	73	50.7	107	KV04_RABIT	P01685 oryctolagus
33	73	50.7	115	KV2A_HUMAN	P01614 homo sapien

34	73	50.7	129	1	KV1X_HUMAN	P04432 homo sapien
35	72	50.0	108	1	KV1L_HUMAN	P01604 homo sapien
36	71	49.3	108	1	KV1E_HUMAN	P01597 homo sapien
37	71	49.3	108	1	KV1N_HUMAN	P01606 homo sapien
38	71	49.3	109	1	KV3B_HUMAN	P01620 mus musculu
39	71	49.3	115	1	KV5I_MOUSE	P01642 mus musculu
40	70	48.6	108	1	KV06_RABIT	P01687 oryctolagus
41	70	48.6	108	1	KV3A_HUMAN	P01618 homo sapien
42	70	48.6	109	1	KV1T_HUMAN	P01612 homo sapien
43	70	48.6	112	1	KV2D_MOUSE	P01629 mus musculu
44	70	48.6	113	1	KV2B_HUMAN	P01615 homo sapien
45	70	48.6	113	1	KV2D_HUMAN	P01617 homo sapien

ALIGNMENTS

```
RESULT 1
ID      KVA4_HUMAN          STANDARD;      PRT;      114 AA.
AC      P01625;
DT      21-JUL-1986 (rel. 01, Created)
DR      01-OCT-1996 (rel. 34, Last sequence update)
DR      15-JUL-1999 (rel. 38, Last annotation update)
DE      Ig kappa chain V-IV region Len.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON      NCBI_TaxID=9606;
RN      [1]
RP      MEDLINE=76004342; PubMed=50995;
RX      Schneider M., Hilschmann N.;
RT      "The primary structure of a monoclonic immunoglobulin-L-chain of
RL      subgroup IV of the kappa type (Bence-Jones protein len).";
RN      [2]
RP      Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RA      Revision to 9.
RA      Salomon A.;
CC      Submitted (AUG-1996) to the SWISS-PROT data bank.
CC      -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR      PIR; A01903; K4HULN.
DR      HSSP; P01789; IMCP.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
KW      Immunoglobulin V region; Bence-Jones protein.
FT      DOMAIN 1 24 40 40
FT      DOMAIN 2 41 55 55
FT      DOMAIN 3 56 62 62
FT      DOMAIN 4 63 94 94
FT      DOMAIN 5 95 101 101
FT      DOMAIN 6 102 113 113
FT      DISULFD 23 94
FT      NON_TER 114 114
SQ      SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;
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Query Match 60.4%; Score 87; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 4,9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGSGTDFLTITSLQAED 29
Db 71 SGGSGTDFLTITSLQAED 88

RESULT 2
ID KVA0_HUMAN STANDARD; PRT; 121 AA.

```

AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combrlato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
CC -I- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
CC -----
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CC -----
CC EMBL: 200023; CAAT7318.1;
DR PIR: A01902; K4HU.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 60.4%; Score 87; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSGDTFTLTISLQAE 29
DB 91 SSGSGDTFTLTISLQAE 108

RESULT 3
KVAB_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combrlato G., Mocikat R., Pohlenz H.D.,

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RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
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CC -----
CC EMBL: 200022; CAAT7317.1;
DR PIR: A01904; K4HUJ1.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AE4 CRC64;

Query Match 60.4%; Score 87; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSGDTFTLTISLQAE 29
DB 91 SSGSGDTFTLTISLQAE 108

RESULT 4
KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RT Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
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CC EMBL: X02990; CAA26733.1; -
CC PIR: A01905; K4H017.
DR HSSP: P01789; 1MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFID 43 134 BY SIMILARITY.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FDD738832 CRC64;

Query Match 60.4%; Score 87; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSGDTFTLTSSLOAED 29
DB 91 SSGSGDTFTLTSSLOAED 108

RESULT 5
KV11_HUMAN STANDARD; PRT; 108 AA.
ID KV11_HUMAN
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE 19 kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups.",
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01868; K1H0H0.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 56.9%; Score 82; DB 1; Length 108;
Best Local Similarity 94.4%; Pred. No. 2.5e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 SSGSGDTFTLTSSLOAED 29
DB 65 SSGSGDTFTLTSSLOPED 82

RESULT 6
KV3J_HUMAN STANDARD; PRT; 116 AA.
ID KV3J_HUMAN
AC P0434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Ig kappa chain V-III region VH precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated within the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
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CC EMBL: X02725; -; NOT_ANNOTATED_CDS.
DR PIR: A01901; K3H0VH.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 FRAMEWORK-3.
FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 110 109 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD5BA3B21929 CRC64;

Query Match 56.9%; Score 82; DB 1; Length 116;
Best Local Similarity 94.4%; Pred. No. 2.7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 SSGSGDTFTLTSSLOAED 29
DB 86 SSGSGDTFTLTSSLOPED 103

RESULT 7
KV11_HUMAN STANDARD; PRT; 117 AA.
ID KV11_HUMAN
AC P01601;

```
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g kappa chain V-I region HK101 precursor (Fragment).
OC Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbits T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RT kappa genes and a pseudogene."
RN Nature 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbits T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
RT recently duplicated human V kappa sequences have diverged by gene
RT conversion."
RL Cell 32:181-189(1983).
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CC -----
CC EMBL; K01322; AAA58930.1; -
CC EMBL; K01324; AAA58932.1; -
CC EMBL; Y00558; CAA23824.1; -
CC PIR; A01881; K1HU11.
CC PIR; A21056; A21056.
CC HSSP; P01607; 1RET.
CC InterPro: IPR003006; Ig_MHC.
CC DR Pfam; PF00047; Ig_V.
CC DR SMART; SM00406; IGV_1.
CC DR SMART; SM00406; IGV_1.
CC KW Immunoglobulin V region; Signal.
CC FT SIGNAL 1 22
CC FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION HK101.
CC FT DOMAIN 23 45 FRAMEWORK-1.
CC FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 57 71 FRAMEWORK-2.
CC FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 79 110 FRAMEWORK-3.
CC FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.
CC FT DISULFID 45 110 BY SIMILARITY.
CC FT NON_TER 117 117
CC SO SEQUENCE 117 AA; 12799 MW; D7D0FF3718CEFF587 CRC64;

Query Match 56.9%; Score 82; DB 1; Length 117;
Best Local Similarity 94.4%; Pred. No. 2.7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SGGSTDFTLTITSLQAD 29
DB 87 SGGSTDFTLTITSLQAD 104

RESULT 8
KV1M_HUMAN STANDARD; PRT; 129 AA.
AC P02431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g kappa chain V-I region Walker precursor.
DE 1g kappa chain V-I region Walker precursor.
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
CC PIR; A01883; K1H0WK.
CC HSSP; P01607; 1RET.
CC InterPro: IPR003006; Ig_MHC.
CC DR Pfam; PF00047; Ig_V.
CC DR SMART; SM00406; IGV_1.
CC KW Immunoglobulin V region; Signal.
CC FT SIGNAL 1 22
CC FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
CC FT DOMAIN 23 45 FRAMEWORK-1.
CC FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 57 71 FRAMEWORK-2.
CC FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 79 110 FRAMEWORK-3.
CC FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
CC FT DOMAIN 120 129 FRAMEWORK-4.
CC FT DISULFID 45 110 BY SIMILARITY.
CC FT NON_TER 129 129
CC SO SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 56.9%; Score 82; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 3.1e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SGGSTDFTLTITSLQAD 29
DB 87 SGGSTDFTLTITSLQAD 104

RESULT 9
KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1g kappa chain V-III region PWM.
DE Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive 1gM anti-gamma globulins."
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR; A01897; K3H0PM.
```


DR HSP; P01789; 2MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DCC6A8ABA86 CRC64;

Query Match 55.6%; Score 80; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 5e-05;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGSTDFLTITISLQED 29
DB 66 SSGSTDFLTITISLQSED 83

RESULT 10
KVLA_MOUSE
ID KVLA_MOUSE STANDARD; PRT; 114 AA.
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region S107A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81241357; PubMed=67888890;
RA Kwan S.-P., Kudikoff S., Seidman J.G., Leder P., Scharif M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
RT chains.";
RL J. Exp. Med. 153:1366-1370(1981).
CC -----
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CC -----
DR EMBL; 029423; AAC00033.1; -.
DR PIR; A01915; KVM57A.
DR HSP; P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 40
FT DOMAIN 41 55
FT DOMAIN 56 62
FT DOMAIN 63 94
FT DOMAIN 95 103
FT DOMAIN 104 113
FT DISULFID 23 94
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12717 MW; 32008EC8E9DE67B CRC64;

Query Match 55.6%; Score 80; DB 1; Length 114;
Best Local Similarity 88.9%; Pred. No. 5.2e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 12 SSGSTDFLTITISLQED 29

DB 71 SSGSTDFLTITISLQVED 88

RESULT 11
KVLA_MOUSE
ID KVLA_MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MPCI1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=83001944; PubMed=6288267;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RT 5'-terminal regions of immunoglobulin variable-region genes.";
RL Cell 29:681-689(1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Mathysseens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes.";
RL Can. J. Biochem. 58:176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MC 11.";
RL Biochem. J. 171:337-347(1978).
CC -1- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END. DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
CC -----
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CC -----
DR EMBL; J00561; AAA38776.1; -.
DR PIR; A01916; KVM511.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 30 149
FT DOMAIN 42 64
FT DOMAIN 65 75
FT DOMAIN 76 90
FT DOMAIN 91 97
FT DOMAIN 98 129
FT DOMAIN 130 138
FT DOMAIN 139 148
FT REPEAT 26 35
FT REPEAT 38 47
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match 55.6%; Score 80; DB 1; Length 149;

Best Local Similarity 88.9%; Pred. No. 7.1e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      12 SSGS GDTFTLT ISS LQAED 29
          |||||
Db      106 SSGS GDTFTFT ISS VQAED 123

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RESULT	12
KV10_HUMAN	
ID	KV10_HUMAN STANDARD; PRT: 108 AA.
AC	P01609;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig kappa chain V-I region Scw.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiinidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=75059271; PubMed=4435756;
RA	Eultz M., Hilschmann N.;
RT	"The primary structure of a human immunoglobulin L-chain of kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides and the complete amino acid sequence.";
RL	Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC	-I' MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC	-I' MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR	PIR: A01875; KIHUSW.
DR	HSSP: P01607; IREI.
DR	InterPro: IPR003006; IG_MHC.
DR	InterPro: IPR003596; IG_V.
DR	Pfam: PF00047; Ig_1.
DR	SMART: SM00406; IGV; 1.
KM	Immunoglobulin V region; Bence-Jones protein.
FT	DOMAIN 1 23 FRAMEWORK-1.
FT	DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 35 49 FRAMEWORK-2.
FT	DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 57 88 FRAMEWORK-3.
FT	DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 98 107 FRAMEWORK-4.
FT	DISULFD 23 88 BY SIMILARITY.
FT	NON_TER 108 108
SO	SEQUENCE 108 AA; 11764 MW; 32CECDDF9644414 CRC64;
QY	12 SGGSTDFLTITSSLOAED 29
DB	65 SGGSTDFLTITSLQPED 82
Query Match	54.9%; Score 79; DB 1; Length 108;
Best Local Similarity	88.9%; Pred. No. 6.9e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0.	
RESULT	13
KV31_HUMAN	
ID	KV31_HUMAN STANDARD; PRT: 115 AA.
AC	P04433;
DT	13-AUG-1987 (Rel. 05, Created)
DT	13-AUG-1987 (Rel. 05, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig kappa chain V-III region VG precursor (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiinidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.

RX MEDLINE=85087932; PubMed=6440122;
 RA Peeth M., Zachau H.G.;
 RI "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus.";
 RL Nucleic Acids Res. 12:9229-9236(1984).

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DR	EMBL: X01668; -, NOT_ANNOTATED_CDS.
DR	PIR: A01900; K3HUVG.
DR	HSSP: P01789; 1MCP.
DR	InterPro: IPR003006; IG_MHC.
DR	InterPro: IPR003596; IG_V.
DR	Pfam: PF00047; IG_1.
DR	SMART: SM00406; IGV_1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL 1 20
FT	CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VS
FT	DOMAIN 21 43 FRAMEOK-1.
FT	DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 55 69 FRAMEOK-2.
FT	DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 77 108 FRAMEOK-3.
FT	DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
FT	DISULFD 43 108 BY SIMILARITY.
FT	NON_TER 115 115
SO	SEQUENCE 115 AA; 12575 MM; 2DE47CDA3A17D555 CRC64;

Search completed: July 15, 2002, 13:23:34
job time: 1450 sec

DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 7399393A95431434A CRC64;

Query Match 54.2%; Score 78; DB 1; Length 108;
Best Local Similarity 88.9%; Pred. No. 9.7e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 SSGGTDFLTLLISSLAED 29
DB 65 SSGGTDFLTLLISSLAED 82

RESULT 15
KV1S_HUMAN STANDARD; PRT; 108 AA.
ID P01611;
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid-9606;
RN [1]
RX MEDLINE-81092279; PubMed-6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of K-type, subgroup I (Bence-Jones protein
RT Wes).";
RL Hoppe-Sevler's 2. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR HSP; P80362; IWTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 54.2%; Score 78; DB 1; Length 108;
Best Local Similarity 88.9%; Pred. No. 9.7e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 SSGGTDFLTLLISSLAED 29
DB 65 SSGGTDFLTLLISSLAED 82

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:22:47 ; Search time 172.49 Seconds

(without alignments)
29,085 Million cell updates/sec

Title: US-09-712-819A-9

Perfect score: 144

Sequence: 1 YERKKRRQRRRSGGDTFTLTISLQAED 29

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	57.6	107	4 Q9UL81	Q9UL81 homo sapien
2	82	56.9	107	4 Q96SA9	Q96SA9 homo sapien
3	82	56.9	108	4 Q9UL77	Q9UL77 homo sapien
4	82	56.9	108	4 Q9UL70	Q9UL70 homo sapien
5	80	55.6	107	11 Q9ER29	Q9ER29 mus musculu
6	80	55.6	109	4 Q9UL85	Q9UL85 homo sapien
7	79	54.9	108	4 Q9UL79	Q9UL79 homo sapien
8	77	53.5	108	4 Q9UL83	Q9UL83 homo sapien
9	74	51.4	109	4 Q9UL78	Q9UL78 homo sapien
10	73	50.7	109	6 Q9N0W5	Q9N0W5 oryctolagus
11	71	49.3	99	11 Q9JL74	Q9JL74 mus musculu
12	70	48.6	104	11 Q9JL82	Q9JL82 mus musculu
13	70	48.6	114	4 Q9UL80	Q9UL80 homo sapien
14	70	48.6	238	11 Q9NM37	Q9NM37 mus musculu
15	69	47.9	233	11 Q9IWS9	Q9IWS9 mus musculu
16	69	47.9	234	11 Q9IWF8	Q9IWF8 mus musculu

17	66	45.8	109	4 Q9UL86	Q9UL86 homo sapien
18	66	45.8	235	11 Q9IWL2	Q9IWL2 mus musculu
19	65	45.1	214	11 Q9RIAS	Q9RIAS mus musculu
20	64	44.4	106	5 Q9UL10	Q9UL10 schistosoma
21	64	44.4	107	11 Q9UL84	Q9UL84 mus musculu
22	64	44.4	116	4 Q96PF6	Q96PF6 homo sapien
23	63	43.8	97	11 Q9JL76	Q9JL76 mus musculu
24	63	43.8	127	11 Q925S9	Q925S9 mus musculu
25	62	43.1	71	15 Q40231	Q40231 human immun
26	62	43.1	101	11 Q9UL78	Q9UL78 mus musculu
27	62	43.1	211	11 Q9IXL0	Q9IXL0 mus musculu
28	61	42.4	111	11 Q920E9	Q920E9 mus musculu
29	60	41.7	72	15 P90117	P90117 human immun
30	60	41.7	109	11 Q920E6	Q920E6 mus musculu
31	60	41.7	298	11 Q9QYF0	Q9QYF0 mus musculu
32	59	41.0	72	15 P90128	P90128 human immun
33	59	41.0	101	15 Q902M7	Q902M7 human immun
34	59	41.0	101	15 Q902L7	Q902L7 human immun
35	58	40.3	72	15 P90118	P90118 human immun
36	58	40.3	101	15 Q902P1	Q902P1 human immun
37	58	40.3	399	10 Q9PYV9	Q9PYV9 oryza sativ
38	57.5	39.9	86	15 Q99BW1	Q99BW1 human immun
39	56	38.9	71	15 Q9IQL4	Q9IQL4 human immun
40	56	38.9	71	15 Q9IQL3	Q9IQL3 human immun
41	56	38.9	71	15 Q9IQK7	Q9IQK7 human immun
42	56	38.9	72	15 Q89731	Q89731 human immun
43	56	38.9	72	15 Q89732	Q89732 human immun
44	56	38.9	72	15 Q89733	Q89733 human immun
45	56	38.9	72	15 Q9WSM3	Q9WSM3 human immun

ALIGNMENTS

RESULT 1
ID Q9UL81 PRELIMINARY: PRT: 107 AA.
AC Q9UL81:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berner S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035033; AAD56269.1; -
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 1
FT NON_TER 107
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 57.6%; Score 83; DB 4; Length 107;

Best Local Similarity 94.4%; Pred. No. 3.2e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SGSGTDFLTITISLQAED 29
Db 65 SGSGTDFLTITISLQAED 82

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RESULT 2
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB6785.1; -.
FT NON_TER 1
FT NON_TER 107
FT SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match
Best Local Similarity 56.9%; Score 82; DB 4; Length 107;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SSGSTDFLTITSSLOAED 29
DB 65 SSGSTDFLTITSSLOPED 82

RESULT 3
Q9UL77 PRELIMINARY; PRT; 108 AA.
ID Q9UL77;
AC Q9UL77;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; 1RET.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match
Best Local Similarity 56.9%; Score 82; DB 4; Length 108;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY 12 SSGSTDFLTITSSLOAED 29
DB 65 SSGSTDFLTITSSLOPED 82

RESULT 4
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; 1RET.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match
Best Local Similarity 56.9%; Score 82; DB 4; Length 108;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SSGSTDFLTITSSLOAED 29
DB 65 SSGSTDFLTITSSLOPED 82

RESULT 5
Q9ERZ9 PRELIMINARY; PRT; 107 AA.
ID Q9ERZ9;
AC Q9ERZ9;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF-a monoclonal antibody."
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF-alpha specific monoclonal antibody."
RL Ti 4 Chun 1 Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
```

```
RA      Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RL      Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR      EMBL; A262753; ANG23804.1; -.  
DR      HSSP; P80362; 1MTL.  
DR      InterPro; IPR003589; Ig.  
DR      InterPro; IPR003006; Ig_MHC.  
DR      Pfam; PF00047; Ig; 1.  
DR      SMART; SM00409; Ig; 1.  
DR      SMART; SM00406; IGV; 1.  
FT      NON_TER 107 107  
SQ      SEQUENCE 107 AA; 11784 MW; 2B15E8A604A26C3 CRC64;  
  
Query Match 55.6%; Score 80; DB 11; Length 107;  
Best Local Similarity 88.9%; Pred. No. 9.2e-05;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 12 SSGSTDFLTITSSLOAED 29  
DB 68 SSGSTDFLTITSSLOAED 85  
|||||  
  
RESULT 6  
Q9UL85 PRELIMINARY; PRT; 109 AA.  
AC Q9UL85;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035029; AAD56265.1; -.  
DR HSSP; P80362; 1MTL.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON_TER 109 109  
FT NON_TER 109 109  
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;  
  
Query Match 55.6%; Score 80; DB 4; Length 109;  
Best Local Similarity 88.9%; Pred. No. 9.4e-05;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 SSGSTDFLTITSSLOAED 29  
DB 65 SSGSTDFLTITSSLOAED 82  
|||||  
  
RESULT 7  
Q9UL79 PRELIMINARY; PRT; 108 AA.  
AC Q9UL79;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
DE (FRAGMENT).
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OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035035; AAD56271.1; -.  
DR HSSP; P01607; 1RET.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON_TER 108 108  
FT NON_TER 108 108  
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;  
  
Query Match 54.9%; Score 79; DB 4; Length 108;  
Best Local Similarity 88.9%; Pred. No. 0.00013;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 12 SSGSTDFLTITSSLOAED 29  
DB 65 SSGSTDFLTITSSLOAED 82  
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RESULT 8  
Q9UL83 PRELIMINARY; PRT; 108 AA.  
AC Q9UL83;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035031; AAD56267.1; -.  
DR HSSP; P80362; 1MTL.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON_TER 108 108  
FT NON_TER 108 108  
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92E8BA96EEA CRC64;  
  
Query Match 53.5%; Score 77; DB 4; Length 108;  
Best Local Similarity 88.9%; Pred. No. 0.00027;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 12 SSGSTDFLTITSSLOAED 29  
DB 65 SSGSTDFLTITSSLOAED 82  
|||||
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```
RESULT 9
Q9UL78 PRELIMINARY: PRT: 109 AA.
AC Q9UL78:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
WU X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
RT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7BE197 CRC64;
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Query Match 51.4%; Score 74; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.0008;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 12 SSGGTDFLTITSSLAQED 29
|||
DB 66 SSGGTDFLTITSRLEPED 83
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RESULT 10
Q9N0W5 PRELIMINARY: PRT: 109 AA.
AC Q9N0W5:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE ANTI-HUMAN A33 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20250927; PubMed=10788485;
RA Rader C., Rlter G., Nathan S., Elia M., Gout I., Jungbluth A.A.,
RA Cohen L.S., Weitz S., Old L.J., Barbas C.F. III.;
RT "The rabbit antibody repertoire as a novel source for the generation
RT of therapeutic human antibodies.";
RL J. Biol. Chem. 275:13668-13676(2000).
DR EMBL: AF245502; AAF68449.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
RT NON_TER 109
SQ SEQUENCE 109 AA; 11323 MW; BDB8396EE75F94FB CRC64;
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Query Match 50.7%; Score 73; DB 6; Length 109;

Best Local Similarity 77.8%; Pred. No. 0.0011;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 12 SSGGTDFLTITSSLAQED 29
|||
DB 65 SSGGTDFLTITGVOAED 82
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RESULT 11
Q9UL74 PRELIMINARY: PRT: 99 AA.
AC Q9UL74:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C;
RX MEDLINE=20448942; PubMed=1092488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206032; AAF69330.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
RT NON_TER 99
SQ SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;
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Query Match 49.3%; Score 71; DB 11; Length 99;
Best Local Similarity 77.8%; Pred. No. 0.0021;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 12 SSGGTDFLTITSSLAQED 29
|||
DB 57 SSGGTDFLTITSTVQAD 74
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RESULT 12
Q9UL82 PRELIMINARY: PRT: 104 AA.
AC Q9UL82:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C;
RX MEDLINE=20448942; PubMed=1092488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206024; AAF69322.1; -.

```


DR HSSP; P01607; 1REL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
SQ SEQUENCE 104 AA; 11360 MW; 5DA8B8FD5F0AA1AE CRC64;

Query Match 48.6%; Score 70; DB 11; Length 104;
Best Local Similarity 77.8%; Pred. No. 0.0032;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 SSGSDFTLTITSSLOAED 29
Db 62 SSGSDFTLTITSSLOAED 79

RESULT 13
Q9UL80

PRELIMINARY; PRT; 114 AA.

AC Q9UL80;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -
DR HSSP; P80362; 1MTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 48.6%; Score 70; DB 4; Length 114;
Best Local Similarity 77.8%; Pred. No. 0.0035;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 SSGSDFTLTITSSLOAED 29
Db 70 SSGSDFTLTITSSLOAED 87

RESULT 14
Q99M37

PRELIMINARY; PRT; 238 AA.

AC Q99M37;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 26.3 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE.-;
RA Strassberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AA02035.1; -
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.
DR InterPro; IPR003600; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 48.6%; Score 70; DB 11; Length 238;
Best Local Similarity 77.8%; Pred. No. 0.0079;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 SSGSDFTLTITSSLOAED 29
Db 89 SSGSDFTLTITSSLOAED 106

RESULT 15
Q91WS9

PRELIMINARY; PRT; 233 AA.

AC Q91WS9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 25.8 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16FB CRC64;

Query Match 47.9%; Score 69; DB 11; Length 233;
Best Local Similarity 72.2%; Pred. No. 0.011;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 12 SSGSDFTLTITSSLOAED 29
Db 84 SSGSDFTLTITSSLOAED 101

Search completed: July 15, 2002, 13:22:48
Job time: 1484 sec

1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 12:57:59 ; Search time 228.39 seconds

(without alignments)
14.104 Million cell updates/sec

Title: US-09-712-819A-9

Perfect score: 144
Sequence: 1 YERKKRRQRRRSGTDFLTITISIAQED 29

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	87	60.4	82	19	AAW62807	Amino acid sequenc
2	87	60.4	94	19	AAW62808	Amino acid sequenc
3	87	60.4	107	20	AAW05269	Antibody 24-31 hum
4	87	60.4	111	15	AAW52059	Light chain variab
5	87	60.4	112	18	AAW27527	Light chain variab
6	87	60.4	113	15	AAW50313	Humanised light ch
7	87	60.4	113	15	AAW50314	Humanised light ch
8	87	60.4	113	17	AAW98489	Humanised 286 anti
9	87	60.4	113	19	AAW42466	Interleukin-5 huma
10	87	60.4	113	21	AAW18857	Amino acid sequenc
11	87	60.4	113	21	AAW18861	Amino acid sequenc

12	87	60.4	113	21	AAW18863	Amino acid sequenc
13	87	60.4	113	21	AAW18869	Amino acid sequenc
14	87	60.4	113	21	AAW18871	Amino acid sequenc
15	87	60.4	113	21	AAW18873	Amino acid sequenc
16	87	60.4	113	21	AAW18879	Amino acid sequenc
17	87	60.4	113	21	AAW18881	Amino acid sequenc
18	87	60.4	113	22	AAW62769	Human HIV-1 monoc
19	87	60.4	114	14	AAW30144	MAB GAH variable r
20	87	60.4	114	15	AAW45605	Monoclonal antibod
21	87	60.4	114	18	AAW15537	Anti-TGF beta-1 sc
22	87	60.4	115	18	AAW27546	Human Ab light cha
23	87	60.4	120	15	AAW61240	Monoclonal antibod
24	87	60.4	120	22	AAW65565	Amino acid sequenc
25	87	60.4	124	20	AAW57181	Amino acid sequenc
26	87	60.4	126	21	AAW77598	Anti-human VEGF re
27	87	60.4	126	22	AAW78867	Anti-human Flt-1 a
28	87	60.4	127	17	AAW06443	HumC3 VL region.
29	87	60.4	131	16	AAW75355	Humanized antibody
30	87	60.4	131	16	AAW70202	Humanized antibody
31	87	60.4	131	20	AAW23779	Light chain variab
32	87	60.4	131	20	AAW23771	Light chain variab
33	87	60.4	131	20	AAW18126	Light chain sequen
34	87	60.4	131	20	AAW18118	Light chain sequen
35	87	60.4	132	21	AAW07966	A light chain vari
36	87	60.4	133	9	AAW80894	V region of L chal
37	87	60.4	133	18	AAW21934	Variable light sub
38	87	60.4	133	20	AAW05264	Antibody 24-31 hum
39	87	60.4	134	20	AAW50690	Human HumA VL Clat
40	87	60.4	135	21	AAW03714	Immunoglobulin kap
41	87	60.4	137	18	AAW10547	Wild type murine a
42	87	60.4	137	18	AAW10544	Humanised murine a
43	87	60.4	137	18	AAW10545	Humanised murine a
44	87	60.4	147	20	AAW34314	Igm antibody CEM 1
45	87	60.4	149	20	AAW34311	Igm antibody CEM 1

ALIGNMENTS

RESULT 1	
AAW62807	standard; Peptide: 82 AA.
XX	
AC	AAW62807;
XX	
DT	23-SEP-1998 (first entry)
XX	
DE	Amino acid sequence of a human antibody fragment.
XX	
KW	Human: immunoglobulin; Ig: transgenic; non-human mammal;
KW	inactivated endogenous Ig locus; B-cell development;
KW	human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW	keppa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW	production: antibody.
XX	
OS	Homo sapiens.
XX	
PN	W09824893-A2.
XX	
PD	11-JUN-1998.
XX	
PF	03-DEC-1997; 97WO-US23091.
XX	
PR	03-DEC-1996; 96US-0759620.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Green I., Jakobovits A., Klapholz S., Kucherlapati R.
XX	
PI	Mendez M.
XX	
DR	WPI: 1998-333314/29.
XX	
PT	New transgenic non-human mammals - having an inactivated

immunoglobulin locus and a near complete human immunoglobulin locus, used for production of human antibodies

Disclosure: Page 78; 128pp; English.

AA62793-822 represent fragments of human antibodies produced by transgenic xenomice, created using the method of the invention. The specification describes a transgenic non-human mammal which has genome modifications that comprise an inactivated endogenous immunoglobulin (Ig) locus, so that the mammal does not display normal B-cell development. The modified genome also has an inserted human heavy chain Ig locus in germline configuration, the human heavy chain Ig locus comprising a human micro constant region and regulatory and switch sequences, human γ -H genes, human D-H genes, and human V-H genes and an inserted human kappa light chain Ig locus in germline configuration, the human kappa light chain Ig locus comprising a human kappa constant region, J-kappa genes, and V-kappa genes, where the number of V-H and V-kappa genes inserted are selected to restore normal B-cell development in the mammal. The transgenic animals have a near complete human Ig locus, including both a human heavy chain locus and a human kappa light chain locus. They can be used for the production of human antibodies when exposed to particular antigens e.g. when exposed to human IL-8, EGFR or TNF- α the mice will produce antibodies to IL-8, EGFR or TNF- α respectively.

Query Match	60.48;	Score 87;	DB 19;	Length 82;
Best Local Similarly	100.08;	Pred. No. 5.6e-05;		
Matches 18; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```

OY      12  S G S G T D F T L T I S S L O A E D 29
          |||||
Db      52  s g s g t d f t l t i s s l o a e d 69

```

RESULT	2
AAW62808	
ID	AAW62808 standard; Peptide; 94 AA.

AAW62808;

DT 23-SEP-1998 (first entry)

DE Amino acid sequence of a human antibody fragment

KW Human; immunoglobulin; Ig; transgenic; non-human mammal;

KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene; KW inactivated endogenous Ig locus; B-cell development;

production; antibody.

OS Homo sapiens.

AA
PN W09824893-A2.

11-JUN-1998.

XX 03-DEC-1997: 97WO-US23091.

XX 03-DEC-1996: 9605-0759620.

XX
PA (ABGE-) ARGENTY TNC

XX	Takehardt & v] anho] r c	Wuchor] aach] t B.
XX		

PI Mendez M;
vv

DR WPI; 1998-333314/29.

PT New transgenic non-human mammals - having an inactivated
PT α 1immunoglobulin locus and a near complete human immunoglobulin locus,
PT used for production of human antibodies

XX
PS Disclosure; Page 79; 128pp; English.

AA66279-822 represent fragments of human antibodies produced by Transgenic Xenomice, created using the method of the invention. The specification describes a transgenic non-human mammal which has genome modifications that comprise an inactivated endogenous immunoglobulin (Ig) locus, so that the mammal does not display normal B-cell development. The modified genome also has an inserted human heavy chain Ig locus in germline configuration, the human heavy chain Ig locus comprising a human micro constant region and regulatory and switch sequences, human J-H genes, human D-H genes, and human V-H genes and an inserted human kappa light chain Ig locus in germline configuration, the human kappa light chain Ig locus comprising a human kappa constant region, J-kappa genes, and V-kappa genes, where the number of V-H and V-kappa genes inserted are selected to restore normal B-cell development in the mammal. The transgenic animals have a near complete human Ig locus, including both a human heavy chain locus and a human kappa light chain locus. They can be used for the production of human antibodies when exposed to particular antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice will produce antibodies to IL-8, EGFR or TNF- alpha respectively.

... SQ Sequence 94 AA;

Query Match	60.48;	Score 87;	DB 19;	Length 94;
Best Local Similarity	100.08;	Pred. No. 6.4e-05;		
Matches 18; Conservative	0;	Mismatches	0;	Gaps 0;

```
QY 12 SSGTDFLTISSLOAED 29
    |||||
Db 52 ssgtdftltissloaed 69
```

RESULT	3
AYAY05269	
ID	AYAY05269 standard; Protein; 107 AA

AA
AC
AAAY05269;

XX	21-JUN-1999 (first entry)
DT	

Antibody 24-31 humanised VL chain sequence.

Antibody 24-31; variable light chain; humanised antibody; gene therapy;

KW graft-versus-host disease; graft rejection; intestinal inflammation;
KW CD40 binding inhibitor; gp95; adonimane aisease; food-related allergy;

KW asthma: lymphoma; immunosuppressant; cellular therapy;
KW reversible obstructive airways disease; airway; transplant rejection

XX Immune response inhibitor; cancer

	Mus sp.
SO	Homo sa
SO	

OS Synthetic.

PN W09912566-A1.
YY

PD 18-MAR-1999

PF 08-SEP-1998; 98WO-US18163.

PR 08-SEP-1997; 97US-0925339.

PA (IDEC-) IDEC PHARM CORP.

PI Black A, Hanna N, Newman RA, Padlan EA;

DR WPI; 1999-229142/19.

PT New humanized antibodies to human gp30
XX
PS Claim 7; Page 84; 122pp; English.

XX This sequence is the variable light chain of a humanised antibody of
CC the invention. The antibody is capable of competing with a murine 24-31
CC antibody for inhibiting CD40 binding to gp39. The humanised antibodies
CC can be used for the treatment of a disease treatable by modulating gp39
CC expression or inhibiting the gp39/CD40 interaction. They can be used for
CC treating e.g. autoimmune diseases such as rheumatoid arthritis, psoriasis
CC multiple sclerosis, diabetes, systemic lupus erythematosus and idiopathic
CC thrombocytopenic purpura (ITP) or non-autoimmune conditions such as
CC graft-versus-host disease (GVHD) or graft rejection. They can also be
CC used for the treatment of reversible obstructive airways disease,
CC intestinal inflammations and allergies (e.g. coeliac disease, Crohn's
CC disease and ulcerative colitis) and food-related allergies (e.g.
CC migraine, rhinitis and eczema), transplant rejection, asthma, leukaemia,
CC or lymphoma. The antibodies can also be used as immunosuppressants, in
CC particular during gene or cellular therapy. They may be used to inhibit
CC humoral and cellular immune responses against viral vectors, e.g.
CC retroviral vectors or adenoviral vectors. The use of such antibodies
CC should enable such cells or vectors to be administered repeatedly, which
CC will facilitate treatment of chronic diseases such as cancers and
CC autoimmune diseases.

XX
SQ Sequence 107 AA;

Query Match 60.4%; Score 87; DB 20; Length 107;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
Db 65 ssgstdflltllsslgaed 82

RESULT 4
AARS2059
ID AARS2059 standard; Protein; 111 AA.

XX AARS2059;

DT 10-OCT-1996 (first entry)

DE Light chain variable region of human KV4B antibody.

XX antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
XX modelling; surface residue; modify.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 1..23

FT Region /label= framework_region_1

FT Region /note= "FR 1"

FT Region /label= complementarity_determining_region_1

FT Region /note= "CDR 1"

FT Region /note= "FR 2"

FT Region /note= "CDR 2"

FT Region /note= "FR 3"

FT Region /note= "CDR 3"

XX EP592106-A1.

XX 13-APR-1994.

XX 07-SEP-1993; 93EP-0307051.

XX 09-SEP-1992; 92US-0942245.

XX (PEDE/) PEDERSEN J T.
PA (IMMUG-) IMMUNOCEN INC.
XX

PI Gullid BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;

DR WPI; 1994-120230/15.

PT Method of resurfacing of rodent antibodies to produce humanised
PT antibody forms - for producing non-human antibodies with improved
PT therapeutic efficiency by presenting human surface on V-region

XX Example 1; Fig 4A; 230pp; English.

XX Modification of a rodent antibody (Ab) or fragment by resurfacing in
CC order to produce a humanised rodent Ab can be determined by calculating
CC homology between murine and human Ab antibody surfaces. In order to test
CC the resurfacing approach of the invention, three humanisation
CC experiments were set up: (1) traditional loop grafting; (2) resurfacing
CC approach using most similar chain; and (3) resurfacing approach using
CC human sequences with most similar surface residues. The Ab used was the
CC murine anti-N901 Ab (see AARS2055). Experiment 3 was carried out using
CC the present sequence which represents the human KV4B Ab light chain
CC variable region with 71 percent homology with anti-N901 Ab. N901/KV4B
CC (AARS2060) was prepd. by resurfacing.

SQ Sequence 111 AA;

Query Match 60.4%; Score 87; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
Db 70 ssgstdflltllsslgaed 87

RESULT 5
AAW27527
ID AAW27527 standard; Protein; 112 AA.

XX AAW27527;

DT 16-DEC-1997 (first entry)

DE Light chain variable region of human CRA2 antibody.

XX Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IGE; Mab; light chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.

OS Homo sapiens.

XX JPO9191886-A.

XX 29-JUL-1997.

XX 19-JAN-1996; 96JP-0024816.

XX 19-JAN-1996; 96JP-0024816.

XX (ASAK) ASAKI BREWERIES LTD.

XX (NIKK-) NIKKA WHISKY KK.

XX (TORI) TORII YAKUHIN KK.

XX (TSUR/) TSURA T.

XX WPI; 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IGE receptor - useful medicinally and have low
PT antigenicity in humans

XX Claim 2; Page 14; 26pp; Japanese.
PS
XX
CC The present sequence, the light chain variable region of the human
CC antibody (Ab) CRA2, was used in the preparation of a humanised or
CC semi-chimeric monoclonal Ab (MAb), comprising complementarity
CC determining regions (CDR) from a murine, anti-human high affinity
CC immunoglobulin E (IgE) receptor, MAb. The humanised, semi-chimeric
CC or chimeric MAb can be used to treat or prevent diseases,
CC specifically allergies, associated with the receptor, and has very
CC low antigenicity in humans.
XX
SQ Sequence 112 AA;

Query Match 60.4%; Score 87; DB 18; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSDFTLTSSLOAED 29
Db 69 sgsqdtltlsslqaed 86

RESULT 6
AAR50313
ID AAR50313 standard; Protein; 113 AA.
XX
AC AAR50313;
XX
DT 05-OCT-1994 (first entry)
XX
DE Humanised light chain variable region PfHzlcl-1.
XX
KW Monoclonal antibody; Plasmodium falciparum; CDR;
KW complementarity determining region; fusion protein;
KW murine; variable; light; heavy; chain; malaria.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Region 24..40
FT /Label= CDR1
FT 56..62
FT /Label= CDR2
FT 95..103
FT Region /Label= CDR3
FT
XX
PN WO9405690-A.
XX
PD 17-MAR-1994.
XX
PE 08-SEP-1993; 93WO-US08435.
XX
PR 09-SEP-1992; 92US-0941654.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (USNA) US SEC OF ARMY.
PA (USNA) US SEC OF NAVY.
XX
PI Charoenvit Y, Hoffman S, Hurlle M, Rosenberg M;
PI Sadoff JC, Sylvester DR, Gross MS;
XX
DR MPI: 1994-101115/12.
DR N-PSDB; AAQ44827.
XX
XX
PT New engineered antibodies and fusion proteins for preventing
PT Plasmodium infection - contg. murine antibody CDR sequences, and
PT corresp. nucleic acid, vectors and transformed cells
XX
PS *Claim 5; Fig 2; 98pp; English.
XX
CC Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28)

CC variable light chain and variable heavy chain sequences
CC derived from murine mAb NFS2 are provided. Murine mAb NFS2,
CC its variable chain peptides, CDRs, functional fragments,
CC Fab fragments, and analogs are useful in prodn. of fusion
CC proteins, esp. engineered antibodies. These prods. are
CC used to protect humans against Plasmodium infections.
XX
SQ Sequence 113 AA;

Query Match 60.4%; Score 87; DB 15; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSDFTLTSSLOAED 29
Db 71 sgsqdtltlsslqaed 88

RESULT 7
AAR50314
ID AAR50314 standard; Protein; 113 AA.
XX
AC AAR50314;
XX
DT 05-OCT-1994 (first entry)
XX
DE Humanised light chain variable region PfHzlcl-2.
XX
KW Monoclonal antibody; Plasmodium falciparum; CDR;
KW complementarity determining region; fusion protein;
KW murine; variable; light; heavy; chain; malaria.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Region 24..40
FT /Label= CDR1
FT 56..62
FT /Label= CDR2
FT 95..103
FT Region /Label= CDR3
FT
XX
PN WO9405690-A.
XX
PD 17-MAR-1994.
XX
PE 08-SEP-1993; 93WO-US08435.
XX
PR 09-SEP-1992; 92US-0941654.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (USNA) US SEC OF ARMY.
PA (USNA) US SEC OF NAVY.
XX
PI Charoenvit Y, Hoffman S, Hurlle M, Rosenberg M;
PI Sadoff JC, Sylvester DR, Gross MS;
XX
DR MPI: 1994-101115/12.
DR N-PSDB; AAQ44828.
XX
XX
PT New engineered antibodies and fusion proteins for preventing
PT Plasmodium infection - contg. murine antibody CDR sequences, and
PT corresp. nucleic acid, vectors and transformed cells
XX
PS Claim 5; Fig 3; 98pp; English.
XX
CC Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28)
CC variable light chain and variable heavy chain sequences
CC derived from murine mAb NFS2 are provided. Murine mAb NFS2,
CC its variable chain peptides, CDRs, functional fragments,
CC Fab fragments, and analogs are useful in prodn. of fusion
CC proteins, esp. engineered antibodies. These prods. are

PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Appelbaum ER, Cook RM;
 XX
 DR WPI; 1998-062853/06.
 DR N-PSDB; AAV03497.
 XX
 PT Use of neutralising antibody to human interleukin-5 - that does not
 PT block binding to receptor alpha chain, to treat e.g. asthma,
 PT allergic rhinitis or atopic dermatitis
 XX
 PS Example 4; Fig 9; 116pp; English.
 XX
 CC This polypeptide comprises a humanised antibody light chain
 CC variable region composed of human LEN framework regions and
 CC complementarily determining regions (see AAM42460-82) derived from
 CC anti-human interleukin-5 (hIL-5) murine monoclonal antibody (MAB)
 CC 2B6 light chain (see AAM42452). It is encoded by a DNA construct
 CC (see AAV03497) in vector pCNI15H2LC1.0 (see AAV03504). The humanised
 CC light chain has been expressed in transfected COS host cells. The
 CC invention provides antibodies, especially altered, chimeric and
 CC humanised antibodies which are characterised by hIL-5 specificity,
 CC neutralising activity and affinity for hIL-5. The antibodies are
 CC useful for treating hIL-5-mediated disorders such as asthma,
 CC allergic rhinitis and atopic dermatitis, and can also be used in
 CC the diagnosis of such conditions by measurement (e.g. by ELISA) of
 CC endogenous hIL-5 levels. Also provided are vectors and transformed
 CC host cells for expression of the novel antibodies.
 XX
 SQ Sequence 113 AA:
 XX
 Query Match 60.4%; Score 87; DB 19; Length 113;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 SSGSTDFLTITSSLOAED 29
 DB 71 ssgstdflltllslgaed 88
 |||||
 RESULT 10
 AAB18857 standard; Protein; 113 AA.
 XX
 AC AAB18857;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of anti-p53 antibody light chain clone 163.2.
 XX
 KM p53; antibody; immune response; vaccine; gene therapy; cancer;
 KM rheumatoid arthritis; coronary heart disease.
 XX
 OS Homo sapiens.
 OS
 PN WO200056770-A1.
 XX
 PD 28-SEP-2000.
 XX
 PE 15-MAR-2000; 2000MO-AU00189.
 XX
 PR 19-MAR-1999; 99AU-0009321.
 XX
 PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
 XX
 PI Ward RL, Coomber DMJ;
 XX
 DR WPI; 2000-638249/61.
 DR N-PSDB; AAA96134.
 XX
 PT 'Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
 PT fragments, useful in treatment and diagnosis of cancer, rheumatoid

PT arthritis and coronary heart disease -
 XX
 PS Claim 30; Page 132; 163pp; English.
 XX
 CC The present sequence represents the light chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibodies
 CC are useful in pharmaceutical compositions, which additionally contain
 CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
 CC or gadolinium. The polypeptide components of the antibodies are useful in
 CC vaccines, for inducing an immune response against a disease in a
 CC vertebrate, for treatment and/or prophylaxis of disease and for detection
 CC purposes. The nucleic acid sequences can be used to detect a disease as
 CC well as for gene therapy and recombinant production of the polypeptides.
 CC In particular, the following can be treated cancer, rheumatoid arthritis
 CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
 CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
 CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
 CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
 CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
 CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
 XX
 SQ Sequence 113 AA:
 XX
 Query Match 60.4%; Score 87; DB 21; Length 113;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 SSGSTDFLTITSSLOAED 29
 DB 71 ssgstdflltllslgaed 88
 |||||
 RESULT 11
 AAB18861 standard; Protein; 113 AA.
 XX
 AC AAB18861;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of anti-p53 antibody light chain clone 163.6.
 XX
 KM p53; antibody; immune response; vaccine; gene therapy; cancer;
 KM rheumatoid arthritis; coronary heart disease.
 XX
 OS Homo sapiens.
 OS
 PN WO200056770-A1.
 XX
 PD 28-SEP-2000.
 XX
 PE 15-MAR-2000; 2000MO-AU00189.
 XX
 PR 19-MAR-1999; 99AU-0009321.
 XX
 PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
 XX
 PI Ward RL, Coomber DMJ;
 XX
 DR WPI; 2000-638249/61.
 DR N-PSDB; AAA96138.
 XX
 PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
 PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
 PT arthritis and coronary heart disease -
 XX
 PS Claim 30; Page 136; 163pp; English.
 XX
 CC The present sequence represents the light chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibodies

CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

XX
SQ Sequence 113 AA:

Query Match 60.4%; Score 87; DB 21; Length 113;

Best Local Similarity 100.0%; Pred. No. 7.8e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSGDTFTLTSSLOAED 29

DB 71 SSGYDFTLTSSlgaed 88

RESULT 12

AAB18863
ID AAB18863 standard; Protein: 113 AA.

XX
AC AAB18863;

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody light chain clone 163.7.

XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;

KW rheumatoid arthritis; coronary heart disease.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT Misc-difference 101

FT /note= "Arg encoded by CCA"

XX
PN WO200056770-A1.

XX
PD 28-SEP-2000.

XX
PF 15-MAR-2000; 2000WO-AU00189.

XX
PR 19-MAR-1999; 99AU-0009321.

XX
PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

XX
PI Ward RL, Coomber DMJ;

XX
PI WPI: 2000-638249/61.

XX
DR N-PSDB; AAA96140.

XX
PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease

XX
PS Claim 30; Page 138; 163pp; English.

XX
CC The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in

CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

XX
SQ Sequence 113 AA:

Query Match 60.4%; Score 87; DB 21; Length 113;

Best Local Similarity 100.0%; Pred. No. 7.8e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSGDTFTLTSSLOAED 29

DB 71 SSGYDFTLTSSlgaed 88

RESULT 13

AAB18869
ID AAB18869 standard; Protein: 113 AA.

XX
AC AAB18869;

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody light chain clone 163.15.

XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;

KW rheumatoid arthritis; coronary heart disease.

XX
OS Homo sapiens.

XX
PN WO200056770-A1.

XX
PD 28-SEP-2000.

XX
PF 15-MAR-2000; 2000WO-AU00189.

XX
PR 19-MAR-1999; 99AU-0009321.

XX
PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

XX
PI Ward RL, Coomber DMJ;

XX
PI WPI: 2000-638249/61.

XX
DR N-PSDB; AAA96146.

XX
PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease

XX
PS Claim 30; Page 144; 163pp; English.

XX
CC The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,

CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
XX
SQ Sequence 113 AA;

Query Match 60.4%; Score 87; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
XXXXXXXXXXXXXXXXXXXX
DB 71 ssgstdflltisslgaed 88

RESULT 14

ID AAB18871 standard; Protein; 113 AA.

AC AAB18871;

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody light chain clone 163.16.

XX p53; antibody; immune response; vaccine; gene therapy; cancer;

KW rheumatoid arthritis; coronary heart disease.

OS Homo sapiens.

PN WO200056770-A1.

PD 28-SEP-2000.

PF 15-MAR-2000; 2000WO-AU00189.

PR 19-MAR-1999; 99AU-0009321.

XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PA Ward RL, Coomber DMJ;

DR WPI: 2000-638249/61.

DR N-PSDB: AAA96148.

XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease -
XX
XX
PS Claim 30; Page 146; 163pp; English.

CC The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
XX
XX
SQ Sequence 113 AA;

Query Match 60.4%; Score 87; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
XXXXXXXXXXXXXXXXXXXX
DB 71 ssgstdflltisslgaed 88

RESULT 15

ID AAB18873 standard; Protein; 113 AA.

AC AAB18873;

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody light chain clone 163.17.

XX p53; antibody; immune response; vaccine; gene therapy; cancer;

KW rheumatoid arthritis; coronary heart disease.

OS Homo sapiens.

PN WO200056770-A1.

PD 28-SEP-2000.

PF 15-MAR-2000; 2000WO-AU00189.

PR 19-MAR-1999; 99AU-0009321.

XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PA Ward RL, Coomber DMJ;

DR WPI: 2000-638249/61.

DR N-PSDB: AAA96150.

XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease -
XX
XX
PS Claim 30; Page 148; 163pp; English.

CC The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
XX
XX
SQ Sequence 113 AA;

Query Match 60.4%; Score 87; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
XXXXXXXXXXXXXXXXXXXX

Db 71 sgsqtdftltlssigaeed 88

Search completed: July 15, 2002, 12:57:59
Job time: 415 sec

1/2
1/2
1/2

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:59:20 ; Search time 75.67 seconds
(without alignments)
9.361 Million cell updates/sec

Title: US-09-712-819A-9

Perfect score: 144

Sequence: 1 YERKKRQRRRRSGGDTFLTTISLQAE D 29

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	60.4	80	3	US-08-554-840-13
2	87	60.4	80	3	US-08-554-840-15
3	87	60.4	107	3	US-08-554-840-2
4	87	60.4	107	4	US-08-525-539A-81
5	87	60.4	112	1	US-07-942-245-30
6	87	60.4	113	1	US-08-467-420A-21
7	87	60.4	113	1	US-08-470-110A-21
8	87	60.4	113	1	US-08-667-769A-21
9	87	60.4	113	2	US-08-940-371-21
10	87	60.4	113	3	US-08-637-647-21
11	87	60.4	113	4	US-08-525-539A-80
12	87	60.4	113	5	PCT-US93-08435-6
13	87	60.4	113	5	PCT-US93-08435-8
14	87	60.4	113	5	PCT-US93-17082A-21
15	87	60.4	114	1	US-08-360-125-6
16	87	60.4	114	2	US-08-450-578-6
17	87	60.4	114	2	US-09-017-628-6
18	87	60.4	114	2	US-09-014-880-6
19	87	60.4	114	4	US-09-025-769B-17
20	87	60.4	115	4	US-09-025-769B-31
21	87	60.4	115	4	US-09-025-769B-49
22	87	60.4	120	1	US-08-026-320A-4
23	87	60.4	127	4	US-08-525-539A-65
24	87	60.4	131	2	US-08-483-636-14
25	87	60.4	131	2	US-08-483-636-58
26	87	60.4	131	2	US-08-483-632-14
27	87	60.4	131	2	US-08-483-632-58

28	87	60.4	133	3	US-08-463-903-4	Sequence 4, Appl
29	87	60.4	133	4	US-07-935-695-4	Sequence 4, Appl
30	87	60.4	135	3	US-08-812-586-46	Sequence 46, Appl
31	87	60.4	155	3	US-08-828-741B-11	Sequence 11, Appl
32	87	60.4	155	4	US-09-160-567-11	Sequence 11, Appl
33	87	60.4	171	3	US-08-463-903-20	Sequence 20, Appl
34	87	60.4	171	4	US-07-935-695-20	Sequence 20, Appl
35	87	60.4	241	2	US-07-916-098A-56	Sequence 56, Appl
36	87	60.4	260	3	US-08-463-903-2	Sequence 2, Appl
37	87	60.4	260	4	US-07-935-695-2	Sequence 2, Appl
38	87	60.4	275	3	US-08-463-903-6	Sequence 6, Appl
39	87	60.4	275	4	US-07-935-695-6	Sequence 6, Appl
40	87	60.4	285	4	US-08-463-903-22	Sequence 22, Appl
41	87	60.4	285	4	US-07-935-695-22	Sequence 22, Appl
42	87	60.4	342	3	US-08-828-741B-6	Sequence 6, Appl
43	87	60.4	342	4	US-09-160-567-6	Sequence 6, Appl
44	87	60.4	495	3	US-08-828-741B-4	Sequence 4, Appl
45	87	60.4	495	4	US-09-160-567-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-554-840-13
Sequence 13, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabli
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Rodin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-13

Query Match 60.4%; Score 87; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;
Qy 12 SGGTDFLTITSLQAE D 29

Db 47 SSGSDFTLTISLQAD 64

RESULT 2

US-08-554-840-15
Sequence 15, Application US/08554840

Patent No. 6001358

GENERAL INFORMATION:

APPLICANT: BLACK, Amelia

APPLICANT: HANNA, Nabli

APPLICANT: PADLAN, Eduardo A.

APPLICANT: NEWMAN, Roland A.

TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,

TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/554,840

FILING DATE: 07-NOV-1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-127

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 80 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-554-840-15

Query Match 60.4%; Score 87; DB 3; Length 80;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGSDFTLTISLQAD 29

Db 47 SSGSDFTLTISLQAD 64

RESULT 3

US-08-554-840-2
Sequence 2, Application US/08554840

Patent No. 6001358

GENERAL INFORMATION:

APPLICANT: BLACK, Amelia

APPLICANT: HANNA, Nabli

APPLICANT: PADLAN, Eduardo A.

APPLICANT: NEWMAN, Roland A.

TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,

TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/554,840

FILING DATE: 07-NOV-1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-127

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-554-840-2

Query Match 60.4%; Score 87; DB 3; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGSDFTLTISLQAD 29

Db 65 SSGSDFTLTISLQAD 82

RESULT 4

US-08-525-539A-81
Sequence 81, Application US/08525539A

Patent No. 6309636

GENERAL INFORMATION:

APPLICANT: DO CUTO, FERNANDO J.R.

APPLICANT: CERIANI, ROBERTO L.

APPLICANT: PETERSON, JERRY A.

TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE

TITLE OF INVENTION: M63 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND

TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/525,539A

FILING DATE: 14-SEP-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: DYLAN, TYLER

REGISTRATION NUMBER: 37,612

REFERENCE/DOCKET NUMBER: 27633-20001.21

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-81

Query Match 60.4%; Score 87; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
DB 65 SSGSTDFLTITSSLOAED 82

RESULT 5
US-07-942-245-30
Sequence 30, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrie, Mion, 21nn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-30

Query Match 60.4%; Score 87; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
DB 71 SSGSTDFLTITSSLOAED 88

RESULT 6
US-08-467-420A-21

Sequence 21, Application US/08467420A
Patent No. 5683892
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TREATMENT OF ALLERGIC DISORDERS
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P. O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,420A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sulton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-420A-21

Query Match 60.4%; Score 87; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
DB 71 SSGSTDFLTITSSLOAED 88

RESULT 7
US-08-470-110A-21
Sequence 21, Application US/08470110A
Patent No. 5693923
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.

TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110A
FILING DATE:
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sulton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-470-110A-21

Query Match 60.4%; Score 87; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SGGSTDTLTITSLQAD 29
|||||

DB 71 SGGSTDTLTITSLQAD 88

RESULT 8
US-08-667-769A-21
Sequence 21, Application US/08667769A
Patent No. 5783184
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,769A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17082
FILING DATE: 22-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sulton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50503
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-667-769A-21

Query Match 60.4%; Score 87; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SGGSTDTLTITSLQAD 29
|||||

DB 71 SGGSTDTLTITSLQAD 88

RESULT 9
US-08-940-371-21
Sequence 21, Application US/08940371
Patent No. 5851525
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,371
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110
FILING DATE:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-940-371-21

Query Match 60.4%; Score 87; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTLSLQAD 29
Db 71 SSGSTDFLTLSLQAD 88

RESULT 10
US-08-637-647-21
Sequence 21, Application US/08637647
Patent No. 6129913
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: McMillan, Lynette J.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P. O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,647
FILING DATE: 19-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/363,131
FILING DATE:
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-637-647-21

Query Match 60.4%; Score 87; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTLSLQAD 29
Db 71 SSGSTDFLTLSLQAD 88

RESULT 11
US-08-525-539A-80
Sequence 80, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-80

Query Match 60.4%; Score 87; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;

```
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 12 SSGGDTFTLTSSLAED 29
Db 71 SSGGDTFTLTSSLAED 88

RESULT 12
PCT-US93-08435-6
; Sequence 6, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-08435-6

Query Match 60.4%; Score 87; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 SSGGDTFTLTSSLAED 29
Db 71 SSGGDTFTLTSSLAED 88

RESULT 13
PCT-US93-08435-8
; Sequence 8, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-08435-8

Query Match 60.4%; Score 87; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 SSGGDTFTLTSSLAED 29
Db 71 SSGGDTFTLTSSLAED 88

RESULT 14
PCT-US95-17082A-21
; Sequence 21, Application PC/TUS9517082A
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chalken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theissen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-0W2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/17082A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/470110
;; FILING DATE: 06-JUN-1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/467420
;; FILING DATE: 06-JUN-1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/363131
;; FILING DATE: 23-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sulton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50282-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5024
;; TELEFAX: 610-270-5090
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US95-17082A-21

Query Match 60.4%; Score 87; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGSDFTLTISLQAE 29
DB 71 SSGSDFTLTISLQAE 88

RESULT 15
US-08-360-125-6
; Sequence 6, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: Kazuhiko MAGAIKE
; APPLICANT: No. 5767246hiko ITO
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Check, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX:
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE: Hybridoma producing human
;; CELL TYPE: antibody GAH
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
;; US-08-360-125-6

Query Match 60.4%; Score 87; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGSDFTLTISLQAE 29
DB 71 SSGSDFTLTISLQAE 88

Search completed: July 15, 2002, 12:59:20
Job time: 391 sec

Db 49 SSGCTDFTLTISLQAE 66
||||| 1 |||||

RESULT 3

S37529 Ig kappa chain V region (V-kappa 4) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37529

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37529

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:226631; NID:g405700; PIDN:CAA81384.1; PID:g405701

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTATAPASSLQAE 29
||||| 1 |||||

RESULT 4

S37535 Ig kappa chain V region (V-kappa 4) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37535

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37535

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:226625; NID:g405712; PIDN:CAA81378.1; PID:g405713

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTATAPASSLQAE 29
||||| 1 |||||

RESULT 5

S37531 Ig kappa chain V region (V-kappa 4) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37531

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37531

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226629; NID:g405704; PIDN:CAA81382.1; PID:g405705
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTATAPASSLQAE 29
||||| 1 |||||

RESULT 6

S37534 Ig kappa chain V region (V-kappa 4) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37534

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37534

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:226626; NID:g405710; PIDN:CAA81379.1; PID:g405711

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTATAPASSLQAE 29
||||| 1 |||||

RESULT 7

S37532 Ig kappa chain V region (V-kappa 4) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37532

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37532

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:226628; NID:g405706; PIDN:CAA81381.1; PID:g405707

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTATAPASSLQAE 29
||||| 1 |||||

RESULT 8

PH0869

Ig kappa chain V region (anti-DNA, H2F) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0869
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosssein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A:Reference number: PH0862; MUID:92078875
A:Accession: PH0869
A:Molecule type: DNA
A:Residues: 1-101 <MAN>
A>Note: residues 28-33 were obtained from Figure 4
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-96/Domain: immunoglobulin homology <IMM>
F:24-40/Region: complementarity-determining 1
F:41-55/Region: framework 2
F:56-62/Region: complementarity-determining 2
F:63-94/Region: framework 3
F:95-101/Region: complementarity-determining 3

Query Match 43.8%; Score 63; DB 2; Length 101;
Best Local Similarity 77.8%; Pred. No. 0.33;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGGTDPATAPASSLOAED 29
||||| | |||||
Db 71 SSGGTDFLTITSSLOAED 88

RESULT 9
B34153
Ig kappa chain V-IV region (Fue) - human
C:Species: Homo sapiens (man)
C:Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jan-2000
C:Accession: B34153
R:Mihasco, E.; Ayadi, H.; Congy, N.; Gendton, M.C.; Roy, J.P.; Heyermann, H.; Frangione
J. Biol. Chem. 264, 21481-21485, 1989
A:Title: Multiple mutations in the variable region of the kappa light chains of three mc
A:Reference number: A34153; MUID:90094313
A:Accession: B34153
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-102 <MIR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 63; DB 2; Length 102;
Best Local Similarity 77.8%; Pred. No. 0.34;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGGTDPATAPASSLOAED 29
||||| | |||||
Db 71 SSGGTDFLTITSSLOAED 88

RESULT 10
A49138
Ig kappa rheumatoid factor variable - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49138
R:Causer, A.; Kupperts, R.; Mierau, R.
Clin. Exp. Immunol. 88, 430-434, 1992
A:Title: A somatically mutated V kappa IV gene encoding a human rheumatoid factor light
A:Reference number: A49138; MUID:92298590
A:Accession: A49138
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-106 <GAU>
A:Cross-references: GB:S37926; NID:g298207; PIDN:AA822366.1; PID:g298208
A>Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI Backbone (NCBIN:106633, NCBIPI:106637)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:20-99/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 63; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 0.35;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGGTDPATAPASSLOAED 29
||||| | |||||
Db 74 SSGGTDFLTITSSLOAED 91

RESULT 11
S30523
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30523
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30523
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z18329
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 63; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGGTDPATAPASSLOAED 29
||||| | |||||
Db 71 SSGGTDFLTITSSLOAED 88

RESULT 12
S30520
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30520
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30520
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z18325
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 63; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGGTDPATAPASSLOAED 29
||||| | |||||
Db 71 SSGGTDFLTITSSLOAED 88

```

RESULT 13
S34003
I9 kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34003
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281
A:Accession: S34003
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

```

```

Query Match          43.8%; Score 63; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

OY 12 SSGCTDATAPASSLOAED 29
      ||||| | |||||
Db 71 SSGCTDTLTITSSLOAED 88

```

RESULT 14

```

S34002
I9 kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34002; S30522
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281
A:Accession: S34002
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:218328
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

```

```

Query Match          43.8%; Score 63; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

OY 12 SSGCTDATAPASSLOAED 29
      ||||| | |||||
Db 71 SSGCTDTLTITSSLOAED 88

```

RESULT 15

```

KARHLN
I9 kappa chain V-IV region (len) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
C:Accession: A01903; F61458
R:Schneider, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975
A:Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette der Subgruppe IV
A:Reference number: A01903; MUID:76004342
A:Accession: A01903
A:Molecule type: protein
A:Residues: 1-114 <SCH>
A:Note: this is the first completely sequenced V region of a new kappa chain subgroup, d
A:Note: the C region of this chain has the Inv (3) marker

```

```

R:Brouet, J.C.; Dellag, K.; Gendron, M.C.; Chevallier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-a
A:Reference number: A61458; MUID:90039128
A:Accession: F61458
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Comment: This is a Bence Jones protein.
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>
F:23-94/Disulfide bonds: #status predicted

```

```

Query Match          43.8%; Score 63; DB 1; Length 114;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

OY 12 SSGCTDATAPASSLOAED 29
      ||||| | |||||
Db 71 SSGCTDTLTITSSLOAED 88

```

```

Search completed: July 15, 2002, 13:01:03
Job time: 469 sec

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:23:34 ; Search time 44.9 Seconds
(without alignments)
25.008 Million cell updates/sec

Title: US-09-712-819A-10

Perfect score: 144

Sequence: 1 YEKRRRQRRRRSGSDTAPASSIAQED 29

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	43.8	114	KV4A_HUMAN	P01625 homo sapien
2	63	43.8	121	KV4O_HUMAN	P06312 homo sapien
3	63	43.8	133	KV4B_HUMAN	P06313 homo sapien
4	63	43.8	134	KV4C_HUMAN	P06314 homo sapien
5	59	41.0	149	KV5A_MOUSE	P01633 mus musculu
6	58	40.3	108	KV10_HUMAN	P01603 homo sapien
7	58	40.3	116	KV3J_HUMAN	P04434 homo sapien
8	58	40.3	117	KV1I_HUMAN	P01601 homo sapien
9	58	40.3	129	KV1M_HUMAN	P04431 homo sapien
10	57	39.6	86	TAT_HV112	P04326 human immun
11	57	39.6	87	TAT_HV11A	P04613 human immun
12	57	39.6	108	KV1O_HUMAN	P01605 homo sapien
13	57	39.6	108	KV1Y_HUMAN	P01607 homo sapien
14	56	38.9	108	KV1C_HUMAN	P80362 homo sapien
15	56	38.9	108	KV3E_HUMAN	P01595 homo sapien
16	56	38.9	109	KV3F_HUMAN	P01624 homo sapien
17	56	38.9	114	KV1A_MOUSE	P01632 mus musculu
18	55	38.2	86	TAT_HV1B1	P04606 human immun
19	55	38.2	86	TAT_HV1BR	P04610 human immun
20	55	38.2	86	TAT_HV1PV	P04607 human immun
21	55	38.2	86	TAT_HV122	P12506 human immun
22	55	38.2	86	TAT_HV1Z6	P04609 human immun
23	55	38.2	108	KV1O_HUMAN	P01609 homo sapien
24	55	38.2	115	KV2A_HUMAN	P01614 homo sapien
25	55	38.2	115	KV3I_HUMAN	P04433 homo sapien
26	55	38.2	654	PC3_YEAST	P32349 saccharomyc
27	54.5	37.8	101	TAT_HV1A2	P04614 human immun
28	54	37.5	101	TAT_HV1S1	P19553 human immun
29	54	37.5	108	KV1P_HUMAN	P01608 homo sapien
30	54	37.5	108	KV1S_HUMAN	P01611 homo sapien
31	54	37.5	136	KV5B_MOUSE	P01634 mus musculu
32	54	37.5	1254	YNCA_CAEEL	P34544 caenorhabd
33	53	36.8	86	TAT_HV1ND	P18804 human immun

34	53	36.8	101	TAT_HV1S3	P19552 human immun
35	53	36.8	621	ULP1_YEAST	Q02724 saccharomyc
36	53	36.8	1239	VI20_EBV	P03189 Epstein-Bar
37	52.5	36.5	100	TAT_STVC2	P17285 chimpanzee
38	52	36.1	86	TAT_HV1H2	P04608 human immun
39	52	36.1	101	TAT_HV1Y2	P35965 human immun
40	52	36.1	108	KV1V_HUMAN	P04430 homo sapien
41	52	36.1	113	KV2B_HUMAN	P01615 homo sapien
42	52	36.1	113	KV2D_HUMAN	P01617 homo sapien
43	52	36.1	113	KV2G_MOUSE	P01631 mus musculu
44	52	36.1	117	KV2E_HUMAN	P06309 homo sapien
45	52	36.1	133	KV2F_HUMAN	P06310 homo sapien

ALIGNMENTS

```
RESULT 1
KV4A_HUMAN          STANDARD:      PRT;      114 AA.
AC P01625;
PT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
  subgroup IV of the kappa type (Bence-Jones protein len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- PIR; A01903; K4HULN.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
KW SMART; SM00406; IGV; 1.
FT DOMAIN 1 23 Bence-Jones protein.
FT DOMAIN 24 40 FRAMEWORK-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 FRAMEWORK-3.
FT DOMAIN 63 94 FRAMEWORK-4.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 113 COMPLEMENTARITY-DETERMINING-4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match          43.8%; Score 63; DB 1; Length 114;
Best Local Similarity 77.8%; Pred. No. 0.084;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
RESULT 2
KV4O_HUMAN          STANDARD:      PRT;      121 AA.
ID KV4O_HUMAN
```

```

AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Moclkat R., Pohlentz H.D.,
RA Zaehau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
CC -I- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; 200023; CAA77318.1; -.
CC PIR; A01902; K4HU.
CC HSSP; P01789; 1MCP.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC SMART; SM00406; IGV; 1.
CC SMART; SM00406; IGV; 1.
KM Immunoglobulin V region: Signal.
FT STGNL 1 20
FT CHAIN 21 >121
FT DOMAIN 21 43
FT DOMAIN 44 60
FT DOMAIN 61 75
FT DOMAIN 76 82
FT DOMAIN 83 114
FT DOMAIN 115 121
FT DISULFID 43 114
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD418BD33974 CRC64;

Query Match 43.8%; Score 63; DB 1; Length 121;
Best Local Similarity 77.8%; Pred. No. 0.09;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SGGSGDTATAPASSLOAED 29
DB 91 SGGSGDTFTLTISLSLOAED 108

RESULT 3
KVAB_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Moclkat R., Pohlentz H.D.,

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RA Zaehau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
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CC -----
CC EMBL; 200022; CAA77317.1; -.
CC PIR; A01904; K4HUJ1.
CC HSSP; P01789; 1MCP.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC SMART; SM00406; IGV; 1.
CC SMART; SM00406; IGV; 1.
KM Immunoglobulin V region: Signal.
FT STGNL 1 20
FT CHAIN 21 133
FT DOMAIN 21 43
FT DOMAIN 44 60
FT DOMAIN 61 75
FT DOMAIN 76 82
FT DOMAIN 83 114
FT DOMAIN 115 122
FT DOMAIN 123 132
FT DISULFID 43 114
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 43.8%; Score 63; DB 1; Length 133;
Best Local Similarity 77.8%; Pred. No. 0.099;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SGGSGDTATAPASSLOAED 29
DB 91 SGGSGDTFTLTISLSLOAED 108

RESULT 4
KVAC_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RT Submitted (OCR-1986) to the EMBL/GenBank/DBJ databases.
CC -----
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CC EMBL; X02990; CAA26733.1; -
CC PIR; A01905; K4H017.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 20
FT DOMAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 43.8%; Score 63; DB 1; Length 134;
Best Local Similarity 77.8%; Pred. No. 0.1;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGSTDTATAPASSLOAED 29
Db 91 SSGSTDTFTLTSSLOAED 108
||||| | |||||

RESULT 5
KV5A_MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MPC11 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=83001944; PubMed=6288267;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RT 5'-terminal regions of immunoglobulin variable-region genes";
RL Cell 29:681-689(1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Matthysens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes";
RL Can. J. Biochem. 58:176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11";
RL Biochem. J. 171:337-347(1978).
CC -I- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.

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CC EMBL; J00561; AAA8776.1; -
CC PIR; A01916; KVM511.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 1 29
FT DOMAIN 42 149 IG KAPPA CHAIN V-V REGION MPC11.
FT DOMAIN 65 75 FRAMEWORK-1.
FT DOMAIN 76 90 FRAMEWORK-2.
FT DOMAIN 91 97 FRAMEWORK-3.
FT DOMAIN 98 129 FRAMEWORK-4.
FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 139 148 FRAMEWORK-4.
FT REPEAT 26 35
FT REPEAT 38 47
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match 41.0%; Score 59; DB 1; Length 149;
Best Local Similarity 72.2%; Pred. No. 0.38;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGSTDTATAPASSLOAED 29
Db 106 SSGSTDTFTLTSSVOAED 123
||||| | |||||

RESULT 6
KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdvision within
RT subgroups";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01868; K1H0HU.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA: 11671 MW: 08D3A6160D8D0618 CRC64:

Query Match 40.3%; Score 58; DB 1; Length 108;
 Best Local Similarity 72.2%; Pred. No. 0.36;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 SSGSGDTATAPASSLOAED 29
 DB 65 SSGSGDTFTLTISLQPED 82

RESULT 7
 KVAL_HUMAN STANDARD; PRT; 116 AA.

AC P04434;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region VH precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 within the V_H locus".
 RL Nucleic Acids Res. 12:9229-9236(1984).
 CC -----
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DR EMBL; X02725; -; NOT_ANNOTATED_CDS.
 DR PIR; A01901; K3H0VH.
 DR HSSP; P01789; 2MCP.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >116 IG KAPPA CHAIN V-II REGION VH.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA: 12757 MW: 51CD55BA53B21929 CRC64:

Query Match 40.3%; Score 58; DB 1; Length 116;
 Best Local Similarity 72.2%; Pred. No. 0.39;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 SSGSGDTATAPASSLOAED 29
 DB 86 SSGSGDTFTLTISLQPED 103

RESULT 8
 KVAL_HUMAN STANDARD; PRT; 117 AA.

AC P01601;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region HK101 precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81098966; PubMed=6779204;
 RA Bentley D.L., Rabbitts T.H.;
 RT "Human immunoglobulin variable region genes -- DNA sequences of two V
 kappa genes and a pseudogene".
 RL Nature 288:730-733(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83129397; PubMed=6402305;
 RA Bentley D.L., Rabbitts T.H.;
 RT "Evolution of immunoglobulin V genes: evidence indicating that
 recently duplicated human V kappa sequences have diverged by gene
 conversion".
 RL Cell 32:181-189(1983).
 CC -----
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DR EMBL; K01322; AA58930.1; -;
 DR EMBL; K01324; AA58932.1; -;
 DR EMBL; V00558; CAA23824.1; -;
 DR PIR; A01881; K1H011.
 DR PIR; A21056; A21056.
 DR HSSP; P01607; 1REI.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION HK101.
 FT DOMAIN 23 45 FRAMEWORK-1.
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 57 71 FRAMEWORK-2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 79 110 FRAMEWORK-3.
 FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA: 12799 MW: D7D0FF3718CE587 CRC64:

Query Match 40.3%; Score 58; DB 1; Length 117;
 Best Local Similarity 72.2%; Pred. No. 0.4;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 SSGSGDTATAPASSLOAED 29
 DB 87 SSGSGDTFTLTISLQPED 104

RESULT 9
 KVAL_HUMAN STANDARD; PRT; 129 AA.

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DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.*;
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC -----
CC EMBL: X00965; CAA25477.1; ALT_TERM.
CC PIR: A01883; K1HWK.
CC HSSP: P01607; 1REI.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam: PF00047; 1g_1.
CC SMART: SM00406; Igv_1.
CC Immunoglobulin V region; Signal.
KW CHAIN
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 40.3%; Score 58; DB 1; Length 129;
Best Local Similarity 72.2%; Pred. No. 0.44;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 12 SSGSGDTATAPASSIQAED 29
DB 87 SSGSGDTFTLTLSLOPED 104

RESULT 10
ID TAT_HV112 STANDARD: PRT; 86 AA.
AC P04326;
DT 20-MAR-1987 (Rel. 04, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177573; PubMed=3008154;
RA Arya S.K., Gallo R.C.;
RT "Three novel genes of human T-lymphotropic virus type III: Immune
RT reactivity of their products with sera from acquired immune

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RT deficiency syndrome patients.*;
RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE ITR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
CC EMBL: M1840; AAA4499.1; -.
CC PIR: A04017; TNLJ12.
CC HIV: M1840; TATSPV12.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam: PF00539; Ttt_1.
CC PRINTS: PR00055; HIVTADOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
KW SEQUENCE 86 AA; 9758 MW; 4DD609414FBE9115 CRC64;

Query Match 39.6%; Score 57; DB 1; Length 86;
Best Local Similarity 50.0%; Pred. No. 0.39;
Matches 13; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 1 YERKKRORRRSGTDAFPASSIQ 26
DB 47 YERKKRORRRAPQSGTHQVSLSKQ 72

RESULT 11
ID TAT_HV1MA STANDARD: PRT; 87 AA.
AC P04613;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11697;
RN [1]
RP MEDLINE=86245056; PubMed=2424612;
RA Allizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.*;
RL Cell 46:63-74(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
CC EMBL: X04415; CAA28015.1; -.
CC HIV: K03456; TAT5MAL.

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DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 87 AA; 10036 MW; 3832412849D5B1CE CRC64;

Query Match 39.6%; Score 57; DB 1; Length 87;
Best Local Similarity 66.7%; Pred. No. 0.39;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 YEKRRRRRRSGSGTDA 18
I | | | | | | | | | |
Db 47 YGKKRRRRRRRRPGNQ 64

RESULT 12

KV1M_HUMAN STANDARD; PRT; 108 AA.
ID P01605;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Iay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=77038198; PubMed=824717;
RX Capra J.D., Klapper D.G.;

RT "Complete amino acid sequence of the variable domains of two human
RT Igm anti-gamma globulins (Iay/Pom) with shared idiotypic
RT specificities.";
RT Scand. J. Immunol. 5:677-684(1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POW-V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01871; KIHOLY.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 39.6%; Score 57; DB 1; Length 108;
Best Local Similarity 72.2%; Pred. No. 0.49;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 12 SSGGTATAPASSLOAED 29
I | | | | | | | | | |
Db 65 SSGGTDTFTTISLQPED 82

RESULT 13
KV1O_HUMAN STANDARD; PRT; 108 AA.
ID

AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;

RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type I-chain, subgroup I (Bence-Jones protein Rel): isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;

RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rel refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01873; KIHORE.
DR PDB: IREI; 17-FEB-84.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
KW DOMAIN 1 23
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 33 38
FT STRAND 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT TURN 70 75
FT STRAND 80 82
FT STRAND 85 90
FT STRAND 98 106
FT STRAND 102 106
FT NON_TER 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8133E118BCE2A CRC64;

Query Match 39.6%; Score 57; DB 1; Length 108;
Best Local Similarity 72.2%; Pred. No. 0.49;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 12 SSGGTATAPASSLOAED 29

DB 65 SSGSGTDTFTTSSLOPED 82

RESULT 14
KVLY_HUMAN STANDARD: PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eultz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers.";
RL Biochemistry 33:1484-1487(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human kappa Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PDB: 1MTL, 01-NOV-94.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 24 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 35 FRAMEWORK-2.
FT DOMAIN 4 49 FRAMEWORK-2.
FT DOMAIN 5 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 6 57 FRAMEWORK-3.
FT DOMAIN 7 88 FRAMEWORK-3.
FT DOMAIN 8 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 9 98 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT CONFLICT 30 31 TN -> SD (IN REF. 2).
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 39.6%; Score 57; DB 1; Length 108;
Best Local Similarity 72.2%; Pred. No. 0.49;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 12 SSGSGTDTAPASSLOAED 29
DB 65 SSGSGTDTFTTSSLOPED 82

RESULT 15
KVLY_HUMAN STANDARD: PRT; 108 AA.
AC P01595;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region BI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=73029807; PubMed=4563064;
RA Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
RT "Principle of antibody structure. The primary structure of a
RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein
RT BI). 3. The complete amino acid sequence and the genetic
RT significance of the variability principles for the mechanism of
RT antibody formation.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR: A01863; KIHUB1.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 24 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 35 FRAMEWORK-2.
FT DOMAIN 4 49 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 56 FRAMEWORK-3.
FT DOMAIN 6 57 FRAMEWORK-3.
FT DOMAIN 7 88 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 8 97 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

Query Match 38.9%; Score 56; DB 1; Length 108;
Best Local Similarity 65.0%; Pred. No. 0.67;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 10 RRSFGTDTAPASSLOAED 29
DB 63 RGSFGTDTFALSISLOPED 82

Search completed: July 15, 2002, 13:23:34
Job time: 1450 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:22:48 ; Search time 172.49 Seconds
(without alignments)
29.085 Million cell updates/sec

Title: US-09-712-819A-10
Perfect score: 144
Sequence: 1 YERKKRRQRRRRSGSDATAPASSIQAED 29

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_humani:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	65	45.1	399	10 Q9FTY9	Q9FTY9 oryza sativ
2	63	43.8	101	15 Q71973	Q71973 human immun
3	62	43.1	71	15 Q40231	Q40231 human immun
4	62	43.1	444	4 Q43284	Q43284 homo sapien
5	62	43.1	1312	4 Q9NR59	Q9NR59 homo sapien
6	62	43.1	1343	4 Q9H7N4	Q9H7N4 homo sapien
7	61	42.4	101	15 Q902I7	Q902I7 human immun
8	60.5	42.0	101	15 Q902I7	Q902I7 human immun
9	60	41.7	72	15 Q69622	Q69622 human immun
10	60	41.7	72	15 P90117	P90117 human immun
11	60	41.7	72	15 P90128	P90128 human immun
12	60	41.7	101	15 Q90MK8	Q90MK8 human immun
13	60	41.7	829	5 Q9NEA9	Q9NEA9 leishmania
14	60	41.7	989	5 Q9YDVO	Q9YDVO drosophila
15	59	41.0	72	15 P901A8	P901A8 human immun
16	59	41.0	86	15 Q9QRB4	Q9QRB4 human immun

17	59	41.0	101	15 Q902M7	Q902M7 human immun
18	59	41.0	107	4 Q9UL81	Q9UL81 homo sapien
19	58.5	40.6	171	5 Q9N870	Q9N870 leishmania
20	58	40.3	71	15 Q71898	Q71898 human immun
21	58	40.3	71	15 Q71805	Q71805 human immun
22	58	40.3	71	15 Q71919	Q71919 human immun
23	58	40.3	71	15 Q71926	Q71926 human immun
24	58	40.3	71	15 Q71932	Q71932 human immun
25	58	40.3	72	15 P90118	P90118 human immun
26	58	40.3	72	15 P90134	P90134 human immun
27	58	40.3	72	15 P90149	P90149 human immun
28	58	40.3	101	15 Q902P1	Q902P1 human immun
29	58	40.3	107	4 Q96SA9	Q96SA9 homo sapien
30	58	40.3	108	4 Q9UL77	Q9UL77 homo sapien
31	58	40.3	108	4 Q9UL70	Q9UL70 homo sapien
32	57	39.6	72	15 Q70495	Q70495 human immun
33	57	39.6	72	15 Q70501	Q70501 human immun
34	57	39.6	72	15 Q70502	Q70502 human immun
35	57	39.6	72	15 Q70504	Q70504 human immun
36	57	39.6	72	15 Q70507	Q70507 human immun
37	57	39.6	72	15 Q70509	Q70509 human immun
38	57	39.6	72	15 Q70510	Q70510 human immun
39	57	39.6	72	15 Q70512	Q70512 human immun
40	57	39.6	72	15 Q70513	Q70513 human immun
41	57	39.6	72	15 Q70515	Q70515 human immun
42	57	39.6	72	15 Q70526	Q70526 human immun
43	57	39.6	72	15 Q70533	Q70533 human immun
44	57	39.6	72	15 Q70539	Q70539 human immun
45	57	39.6	72	15 P90158	P90158 human immun

ALIGNMENTS

RESULT 1
Q9FTY9
ID Q9FTY9 PRELIMINARY: PRT: 399 AA.
AC Q9FTY9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE RECEPTOR SER/THR PROTEIN KINASE.
GN P0436E04.9.
OS Oryza sativa (Rice).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
OC Spermatophyta: Magnoliophyta, Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzae; Oryza.
OC Euphorbiaceae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPONBARE;
RA Saeki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(Ga3) genomic DNA, chromosome 1, PAC
clone: P0436E04.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002818; BAB16326.1; -;
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR InterPro: IPR01245; Tyr_Pkinase.
DR Pfam: PF00069; Pkinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 399 AA; 45329 MW; E2D92FE1F6DAAC7B CRC64;

Query Match 45.1%; Score 65; DB 10; Length 399;
Best Local Similarity 65.0%; Pred. No. 0.31;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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OY 1 YEKRRRRRRSGSTDATA 20
    1 | | | | | | | | | |
Db 54 YRSKRRRRRSGSSTATA 73

RESULT 2
ID 071973 PRELIMINARY: PRT: 101 AA.
AC 071973;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HIV-1NC;
RX MEDLINE=98440562; PubMed=9765443;
RA Mwaengo D.M., Novembre F.J.;
RT "Molecular cloning and characterization of viruses isolated from
RT chimpanzees with pathogenic human immunodeficiency virus type 1
RT infections."
RT J. Virol. 72:8976-8987(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-HIV-1NC;
RA Mwaengo D.M., Novembre F.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AF049495; AAC68854.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PS00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11439 MW; C13CC065D9DA888 CRC64;

Query Match 43.8%; Score 63; DB 15; Length 101;
Best Local Similarity 44.1%; Pred. No. 0.14;
Matches 15; Conservative 4; Mismatches 9; Indels 6; Gaps 1;

OY 1 YEKRRRRRRSGSTDA-----TAPASSLOAE 28
    1 | | | | | | | | | |
Db 47 YGKRRRRRRAPQSQAHQASLSSEPTSQLRCD 80

RESULT 3
ID 040231 PRELIMINARY: PRT: 71 AA.
AC 040231;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HE93-A3TAT;
RX MEDLINE=97335179; PubMed=9191845;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Destroiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tail genes derived from individuals with different rates of
RT disease progression.";
```

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RL Virology 232:319-331(1997).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AF000529; AAB62528.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON-TER 71
SQ SEQUENCE 71 AA; 8162 MW; 5AFB3242EB2321B3 CRC64;

Query Match 43.1%; Score 62; DB 15; Length 71;
Best Local Similarity 78.9%; Pred. No. 0.14;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

OY 1 YEKRRRRRRS--GSSTD 17
    1 | | | | | | | | | |
Db 47 YGKRRRRRRSPQSGSTD 65

RESULT 4
ID 043284 PRELIMINARY: PRT: 444 AA.
AC 043284;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE LAK-4p.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOID;
RA Abe Y., Takaoka Y.;
RT "LAK-4 clone from the membrane lymphotoxin expressing subtraction
RT library."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB002405; BAA24179.2; -.
DR InterPro: IPR000515; BPD_transp.
DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN_1.
SQ SEQUENCE 444 AA; 50427 MW; DD4053A374A00FA1 CRC64;

Query Match 43.1%; Score 62; DB 4; Length 444;
Best Local Similarity 46.4%; Pred. No. 0.91;
Matches 13; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 YEKRRRRRRSGSTDATAPASSLOAE 28
    1 | | | | | | | | | |
Db 414 YEKREERSRYGTTEEAAPALITDE 441

RESULT 5
ID 09NR59 PRELIMINARY: PRT: 1312 AA.
AC 09NR59;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE SER/ARG-RICH PRE-MRNA SPLICING FACTOR SR-A1.
GN SR-A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Scorilas A., Kyriakopoulou L., Katsaros D., Diamandis E.P.;
```

RT 'Cloning of a gene (SR-A1) encoding a new member of the human Ser/Arg-
 rich family of pre-mRNA splicing factors.';
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF254411; AAF87552.1; -;
 DR InterPro: IPR002965; P_rich_extensn.
 DR PRINTS: PRO1217; PRICEXTENSN.
 SQ SEQUENCE 1312 AA; 139269 MW; 0CB1C87C963C52BD CRC64;

Query Match 43.1%; Score 62; DB 4; Length 1312;
 Best Local Similarity 53.8%; Pred. No. 2.8;
 Matches 14; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 3 RKKRRQRRSGSGTDPAPASSLQAE 28
 DB 603 RKKRRRRRSASPPATSSSSSRRE 628

RESULT 6
 O9H7N4 PRELIMINARY; PRT; 1343 AA.
 AC O9H7N4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE FLJ00034 PROTEIN (FRAGMENT).
 GN FLJ00034.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RA Ohara O., Nagase T., Kikuno R., Okumura K.;
 RT 'The nucleotide sequence of a long cDNA clone isolated from human
 spleen.';
 RT Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AK024444; BAB15734.1; -;
 DR InterPro: IPR002965; P_rich_extensn.
 DR PRINTS: PRO1217; PRICEXTENSN.
 FT NON_TER
 SQ SEQUENCE 1343 AA; 142483 MW; FA7ABD473C74688C CRC64;

Query Match 43.1%; Score 62; DB 4; Length 1343;
 Best Local Similarity 53.8%; Pred. No. 2.8;
 Matches 14; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 OY 3 RKKRRQRRSGSGTDPAPASSLQAE 28
 DB 634 RKKRRRRRSASPPATSSSSSRRE 659

RESULT 7
 O71968 PRELIMINARY; PRT; 101 AA.
 AC O71968;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
 GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIV-1JC;
 RX MEDLINE=98440562; PubMed=9765443;
 RA Mwaengo D.M., Novembre F.J.;
 RT 'Molecular cloning and characterization of viruses isolated from
 chimpanzees with pathogenic human immunodeficiency virus type 1

RT infections.';
 RL J. Virol. 72:8976-8987(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIV-1JC;
 RA Mwaengo D.M., Novembre F.J.;
 RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
 CC -1 FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER (BY SIMILARITY).
 CC EMBL: AF049494; AAC68845.1; -;
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat.1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
 SQ SEQUENCE 101 AA; 11552 MW; DE1EFC34D9CDB8 CRC64;

Query Match 42.4%; Score 61; DB 15; Length 101;
 Best Local Similarity 44.1%; Pred. No. 0.28;
 Matches 15; Conservative 3; Mismatches 10; Indels 6; Gaps 1;
 OY 1 YERKKRRQRRSGSGTDA-----TAPASSLQAE 28
 DB 47 YGKKRRQRRRPGSGAHOASLSSEQPTSQLRGD 80

RESULT 8
 O902L7 PRELIMINARY; PRT; 101 AA.
 AC O902L7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TAT PROTEIN.
 GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ARMA037;
 RA Carr J.K., Avila M., Gomez-Carrillo M., Salomon H., Hierholzer J.,
 RA Matanaveeradej V., Pando M., Negrete M., Russell K.L., Sanchez J.,
 RA Bix D.L., Andrade R., Vinolas J., McCutchan F.E.;
 RT 'Diverse BF Recombinants have spread widely since the introduction of
 HIV-1 into South America.';
 RL AIDS 0:0-0(2001).
 DR EMBL: AY037277; AAL12713.1; -;
 SQ SEQUENCE 101 AA; 11572 MW; 13A12A179D2EF930 CRC64;

Query Match 42.0%; Score 60.5; DB 15; Length 101;
 Best Local Similarity 39.0%; Pred. No. 0.33;
 Matches 16; Conservative 1; Mismatches 7; Indels 17; Gaps 1;
 OY 1 YERKKRRQRRSGSGT-----DAPASS 24
 DB 47 YGKKRRQRRRSPGSGIHOPIKOPIPQAGDPTGPKS 87

RESULT 9
 O69622 PRELIMINARY; PRT; 72 AA.
 AC O69622;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
 GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=RI_22;
RX MEDLINE=95264414; PubMed=7745674;
RA Diaz R.S., Sabino E.C., Mayer A., Mosley J.W., Busch M.P.;
RT "Dual human immunodeficiency virus type 1 infection and recombination
in a dually exposed transfusion recipient. The Transfusion Safety
Study Group.";
RL J. Virol. 69:3273-3281(1995).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: U11185; AAB78871.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER
SQ SEQUENCE 72 AA; 8331 MW; 4CD2C4425E67286 CRC64;

Query Match 41.7%; Score 60; DB 15; Length 72;
Best Local Similarity 53.8%; Pred. No. 0.27;
Matches 14; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 YEKRRRRRRSGCTDATAAPASSIQ 26
DB 47 YGKRRRRRRAPQGNQHVSLSKQ 72

RESULT 10
P90117 PRELIMINARY; PRT; 72 AA.
AC P90117;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT VE3;
RA Quinones-Mateu M.E., Domingo E.;
RT "Point mutant frequency and intrasubtype B recombination lead
RT Venezuelan HIV-1 genetic diversities.";
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: U80463; AAB39113.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER
SQ SEQUENCE 72 AA; 8214 MW; F79D7B8D0205EEB0 CRC64;

Query Match 41.7%; Score 60; DB 15; Length 72;
Best Local Similarity 64.7%; Pred. No. 0.27;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 YEKRRRRRRSGCTD 17
DB 47 YGKRRRRRRASGSE 63

RESULT 11
P90128 PRELIMINARY; PRT; 72 AA.
ID P90128;
AC P90128;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT VE18;
RA Quinones-Mateu M.E., Domingo E.;
RT "Point mutant frequency and intrasubtype B recombination lead
RT Venezuelan HIV-1 genetic diversities.";
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: U80477; AAB39127.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER
SQ SEQUENCE 72 AA; 8337 MW; 4D0AED1145E6645C CRC64;

Query Match 41.7%; Score 60; DB 15; Length 72;
Best Local Similarity 53.8%; Pred. No. 0.27;
Matches 14; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 YEKRRRRRRSGCTDATAAPASSIQ 26
DB 47 YGKRRRRRRSPQSQTHQVSLSKQ 72

RESULT 12
O90MK8 PRELIMINARY; PRT; 101 AA.
ID O90MK8;
AC O90MK8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ARMA159;
RA Carr J.K., Avila M., Gomez-Carrillo M., Salomon H., Hierholzer J.,
RA Matanaveceradej V., Pando M., Negrete M., Russell K., Sanchez J.,
RA Bix D., Andrade R., Vinales J., McCutchan F.;
RT "Diverse BF recombinants have spread widely since the introduction of
RT HIV-1 into South America.";
RL AIDS 0:0-0(2001).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ARMA159;
RA Carr J.K., Avila M., Gomez-Carrillo M., Salomon H., Hierholzer J.,
RA Matanaveceradej V., Pando M., Negrete M., Russell K., Sanchez J.,
RA Bix D., Andrade R., Vinales J., McCutchan F.;
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF385936; AAK69333.1; -.
SQ SEQUENCE 101 AA; 11416 MW; 360605029A87A327 CRC64;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:57:59 ; Search time 228.39 Seconds

(without alignments)
14.104 Million cell updates/sec

Title: US-09-712-819A-10

Perfect score: 144
Sequence: 1 YERKKRRQRSGGTADATAPASSLOAED 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802:*
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2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
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6: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
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11: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
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21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	43.8	82	19	AAW62807
2	63	43.8	94	19	AAW62808
3	63	43.8	107	20	AAV05269
4	63	43.8	111	15	AAW52059
5	63	43.8	112	18	AAW27527
6	63	43.8	113	15	AAW50313
7	63	43.8	113	15	AAW50314
8	63	43.8	113	17	AAW98489
9	63	43.8	113	19	AAW42466
10	63	43.8	113	21	AAW18857
11	63	43.8	113	21	AAW18861

12	63	43.8	113	21	AAW18863	Amino acid sequenc
13	63	43.8	113	21	AAW18869	Amino acid sequenc
14	63	43.8	113	21	AAW18871	Amino acid sequenc
15	63	43.8	113	21	AAW18873	Amino acid sequenc
16	63	43.8	113	21	AAW18879	Amino acid sequenc
17	63	43.8	113	21	AAW18881	Amino acid sequenc
18	63	43.8	113	22	AAW62769	Human HIV-1 monoclonal antibody
19	63	43.8	114	14	AAW30144	Human HIV-1 monoclonal antibody
20	63	43.8	114	15	AAW45605	Human HIV-1 monoclonal antibody
21	63	43.8	114	18	AAW15537	Human HIV-1 monoclonal antibody
22	63	43.8	115	18	AAW27546	Human HIV-1 monoclonal antibody
23	63	43.8	120	15	AAW61240	Human HIV-1 monoclonal antibody
24	63	43.8	120	22	AAW65565	Human HIV-1 monoclonal antibody
25	63	43.8	124	20	AAW51811	Human HIV-1 monoclonal antibody
26	63	43.8	126	21	AAW77598	Human HIV-1 monoclonal antibody
27	63	43.8	126	22	AAW78867	Human HIV-1 monoclonal antibody
28	63	43.8	127	17	AAW06443	Human HIV-1 monoclonal antibody
29	63	43.8	131	16	AAW53555	Human HIV-1 monoclonal antibody
30	63	43.8	131	16	AAW70202	Human HIV-1 monoclonal antibody
31	63	43.8	131	20	AAW23779	Human HIV-1 monoclonal antibody
32	63	43.8	131	20	AAW23771	Human HIV-1 monoclonal antibody
33	63	43.8	131	20	AAW18126	Human HIV-1 monoclonal antibody
34	63	43.8	131	20	AAW18118	Human HIV-1 monoclonal antibody
35	63	43.8	132	21	AAW07966	Human HIV-1 monoclonal antibody
36	63	43.8	132	9	AAW80894	Human HIV-1 monoclonal antibody
37	63	43.8	133	18	AAW21934	Human HIV-1 monoclonal antibody
38	63	43.8	133	20	AAW05264	Human HIV-1 monoclonal antibody
39	63	43.8	134	20	AAW50690	Human HIV-1 monoclonal antibody
40	63	43.8	135	21	AAW05714	Human HIV-1 monoclonal antibody
41	63	43.8	137	18	AAW10547	Human HIV-1 monoclonal antibody
42	63	43.8	137	18	AAW10544	Human HIV-1 monoclonal antibody
43	63	43.8	137	18	AAW10545	Human HIV-1 monoclonal antibody
44	63	43.8	147	20	AAW34314	Human HIV-1 monoclonal antibody
45	63	43.8	149	20	AAW34311	Human HIV-1 monoclonal antibody

ALIGNMENTS

AAW62807	1	AAW62807	standard; Peptide: 82 AA.
XX	XX	XX	XX
AC	AAW62807;	XX	XX
XX	XX	XX	XX
DT	23-SEP-1998 (first entry)	XX	XX
XX	XX	XX	XX
DE	Amino acid sequence of a human antibody fragment.	XX	XX
XX	Human; immunoglobulin; Ig; transgenic; non-human mammal;	XX	XX
KW	inactivated endogenous Ig locus; B-cell development;	XX	XX
KW	human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;	XX	XX
KW	kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;	XX	XX
KW	production; antibody.	XX	XX
OS	Homo sapiens.	XX	XX
XX	XX	XX	XX
PN	W09824893-A2.	XX	XX
XX	XX	XX	XX
PD	11-JUN-1998.	XX	XX
XX	XX	XX	XX
PF	03-DEC-1997; 97WO-US3091.	XX	XX
XX	XX	XX	XX
PR	03-DEC-1996; 96US-0759620.	XX	XX
XX	XX	XX	XX
PA	(ABGE-) ABGENIX INC.	XX	XX
XX	XX	XX	XX
PI	Green L, Jakobovits A, Klapholz S, Kuchelapatti R;	XX	XX
XX	Mendez M;	XX	XX
DR	WPI; 1998-333314/29.	XX	XX
XX	XX	XX	XX
PT	New transgenic non-human mammals - having an inactivated	XX	XX

PT immunoglobulin locus and a near complete human immunoglobulin locus,
PT used for production of human antibodies
XX
XX
PS Disclosure: Page 78; 128pp; English.
XX
XX AAM62793-822 represent fragments of human antibodies produced by
CC transgenic Xenomice, created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in
CC germ-line configuration, the human heavy chain Ig locus comprising a human
CC micro constant region and regulatory and switch sequences, human J-H
CC genes, human D-H genes, and human V-H genes and an inserted human kappa
CC light chain Ig locus in germ-line configuration, the human kappa light
CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC and V-kappa genes, where the number of V-H and V-kappa genes inserted
CC are selected to restore normal B-cell development in the mammal. The
CC transgenic animals have a near complete human Ig locus, including both a
CC human heavy chain locus and a human kappa light chain locus. They can
CC be used for the production of human antibodies when exposed to
CC particular antigens e.g. when exposed to human IL-8, EGF or TNF- alpha
CC the mice will produce antibodies to IL-8, EGF or TNF- alpha
CC respectively.
XX
XX
SQ Sequence 82 AA:

Query Match 43.8%; Score 63; DB 19; Length 82;
Best Local Similarity 77.8%; Pred. No. 0.2;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGGDTATAPASSLOAED 29
||||| | |||||
Db 52 sgsydflltllsigaed 69

RESULT 2
AAM62808
ID AAM62808 standard; Peptide: 94 AA.
XX
AC AAM62808;
XX
DT 23-SEP-1998 (first entry)
XX
XX Amino acid sequence of a human antibody fragment.
XX
DE Human; immunoglobulin: Ig; transgenic; non-human mammal;
XX Inactivated endogenous Ig locus; B-cell development;
KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW production; antibody.
XX
XX Homo sapiens.
OS
XX
PN WO9824893-A2.
XX
PD 11-JUN-1998.
XX
PF 03-DEC-1997; 97WO-US23091.
XX
PR 03-DEC-1996; 96US-0759620.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Green L, Jakobovits A, Klapholz S, Kucherlapati R;
PI Mendez W;
XX
XX WPI: 1998-333314/29.
DR
XX
XX New transgenic non-human mammals - having an inactivated
PT immunoglobulin locus and a near complete human immunoglobulin locus,
PT used for production of human antibodies

XX
XX
PS Disclosure: Page 79; 128pp; English.
XX
XX
XX AAM62793-822 represent fragments of human antibodies produced by
CC transgenic Xenomice, created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in
CC germ-line configuration, the human heavy chain Ig locus comprising a human
CC micro constant region and regulatory and switch sequences, human J-H
CC genes, human D-H genes, and human V-H genes and an inserted human kappa
CC light chain Ig locus in germ-line configuration, the human kappa light
CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC and V-kappa genes, where the number of V-H and V-kappa genes inserted
CC are selected to restore normal B-cell development in the mammal. The
CC transgenic animals have a near complete human Ig locus, including both a
CC human heavy chain locus and a human kappa light chain locus. They can
CC be used for the production of human antibodies when exposed to
CC particular antigens e.g. when exposed to human IL-8, EGF or TNF- alpha
CC the mice will produce antibodies to IL-8, EGF or TNF- alpha
CC respectively.
XX
XX
SQ Sequence 94 AA:

Query Match 43.8%; Score 63; DB 19; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGGDTATAPASSLOAED 29
||||| | |||||
Db 52 sgsydflltllsigaed 69

RESULT 3
AAY05269
ID AAY05269 standard; Protein: 107 AA.
XX
AC AAY05269;
XX
DT 21-JUN-1999 (first entry)
XX
XX Antibody 24-31 humanised VL chain sequence.
XX
DE Antibody 24-31 variable light chain; humanised antibody; gene therapy;
XX CD40 binding inhibitor; gp39; autoimmune disease; food-related allergy;
KW graft-versus-host disease; graft rejection; intestinal inflammation;
KW reversible obstructive airways disease; allergy; transplant rejection;
KW asthma; leukaemia; lymphoma; immunosuppressant; cellular therapy;
KW immune response inhibitor; cancer.
XX
XX Mus sp.
OS
XX Homo sapiens.
OS
XX Synthetic.
XX
PN WO9912566-A1.
XX
PD 18-MAR-1999.
XX
PF 08-SEP-1998; 98WO-US18163.
XX
PR 08-SEP-1997; 97US-0925339.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Black A, Hanna N, Newman RA, Padlan EA;
PI WPI: 1999-229142/19.
XX
XX
XX New humanized antibodies to human gp30
PT
XX
XX Claim 7; Page 84; 122pp; English.

XX This sequence is the variable light chain of a humanised antibody of
 CC the invention. The antibody is capable of competing with a murine 24-31
 CC antibody for inhibiting CD40 binding to gp39. The humanised antibodies
 CC can be used for the treatment of a disease treatable by modulating gp39
 CC expression or inhibiting the gp39/CD40 interaction. They can be used for
 CC treating e.g. autoimmune diseases such as rheumatoid arthritis, psoriasis
 CC multiple sclerosis, diabetes, systemic lupus erythematosus and idiopathic
 CC thrombocytopenic purpura (ITP) or non-autoimmune conditions such as
 CC graft-versus-host disease (GVHD) or graft rejection. They can also be
 CC used for the treatment of reversible obstructive airways disease,
 CC intestinal inflammations and allergies (e.g. coeliac disease, Crohn's
 CC disease and ulcerative colitis) and food-related allergies (e.g.
 CC migraine, rhinitis and eczema), transplant rejection, asthma, leukaemia,
 CC or lymphoma. The antibodies can also be used as immunosuppressants, in
 CC particular during gene or cellular therapy. They may be used to inhibit
 CC humoral and cellular immune responses against viral vectors, e.g.
 CC retroviral vectors or adenoviral vectors. The use of such antibodies
 CC should enable such cells or vectors to be administered repeatedly, which
 CC will facilitate treatment of chronic diseases such as cancers and
 CC autoimmune diseases.

XX Sequence 107 AA:

Query Match 43.8%; Score 63; DB 20; Length 107;
 Best Local Similarity 77.8%; Pred. No. 0.27;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGSCTDATAPASSLQAE 29
 Db 65 ssgsctdftlisslqaed 82

RESULT 4

AAR52059
 ID AAR52059 standard; Protein: 111 AA.

AC AAR52059;

DT 10-OCT-1996 (first entry)

DE Light chain variable region of human KV4B antibody.

XX antibody: humanised; murine: human; heavy chain: light; variable;
 KW framework region: complementarity determining region; reshaping;
 KW modelling; surface residue; modify.

XX Homo sapiens.

OS
 FH Key Location/Qualifiers
 FT Region 1.23
 FT /label= framework_region_1
 FT /note= "FR 1"

FT Region 24..40
 FT /label= complementarity_determining_region_1
 FT /note= "CDR 1"

FT Region 41..55
 FT /note= "FR 2"

FT Region 56..62
 FT /note= "CDR 2"

FT Region 63..95
 FT /note= "FR 3"

FT Region 96..104
 FT /note= "CDR 3"

XX EP592106-A1.

XX 13-APR-1994.

XX 07-SEP-1993; 93EP-0307051.

XX 09-SEP-1992; 92US-0942245.

XX (PEDE/) PEDERSEN J T.
 PA (IMMU-) IMMUNOGEN INC.
 XX GUILD BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ.
 DR WPI: 1994-120230/15.

PT Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved
 PT therapeutic efficiency by presenting human surface on V-region

XX Example 1; Fig 4A; 230pp; English.

XX Modification of a rodent antibody (Ab) or fragment by resurfacing in
 CC order to produce a humanised rodent Ab can be determined by calculating
 CC homology between murine and human Ab antibody surfaces. In order to test
 CC the resurfacing approach of the invention, three humanisation
 CC experiments were set up: (1) traditional loop grafting; (2) resurfacing
 CC approach using most similar chain; and (3) resurfacing approach using
 CC human sequences with most similar surface residues. The Ab used was the
 CC murine anti-N901 Ab (see AAR52055). Experiment 3 was carried out using
 CC the present sequence which represents the human KV4B Ab light chain
 CC variable region with 71 percent homology with anti-N901 Ab. N901/KV4B
 CC (AAR52060) was prepd. by resurfacing.

XX Sequence 111 AA;

Query Match 43.8%; Score 63; DB 15; Length 111;
 Best Local Similarity 77.8%; Pred. No. 0.28;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGSCTDATAPASSLQAE 29
 Db 70 ssgsctdftlisslqaed 87

RESULT 5

AAM27527
 ID AAM27527 standard; Protein: 112 AA.

AC AAM27527;

DT 16-DEC-1997 (first entry)

DE Light chain variable region of human CRA2 antibody.

XX Complementarity determining region; CDR; murine; mouse; human;
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
 KW IgE; Mab; light chain; variable region; humanised; semi-chimeric;
 KW chimeric; treatment; prevention; disease; allergy; CRA2.

XX Homo sapiens.

PN JP09191886-A.

PD 29-JUL-1997.

PF 19-JAN-1996; 96JP-0024816.

PR 19-JAN-1996; 96JP-0024816.

XX (ASAK) ASAKI BREWERIES LTD.

PA (NIKK-) NIKKA WHISKY KK.

PA (TORI) TORII YAKUHAN KK.

XX (TSUR/) TSURA T.

XX WPI: 1997-429186/40.

PT Humanised, semi-chimeric and chimeric antibodies against human
 PT high-affinity IgE receptor - useful medicinally and have low
 PT antigenicity in humans

PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI Appelbaum ER, Cook RM;
 XX
 DR WPI: 1998-062853/06.
 DR N-PSDB; AA03497.
 XX
 PT Use of neutralising antibody to human interleukin-5 - that does not
 PT block binding to receptor alpha chain, to treat e.g. asthma,
 PT allergic rhinitis or atopic dermatitis
 XX
 PS Example 4; Fig 9; 116pp; English.
 XX
 CC This polypeptide comprises a humanised antibody light chain
 CC variable region composed of human LEN framework regions and
 CC complementarity determining regions (see AA42460-62) derived from
 CC anti-human interleukin-5 (hIL-5) murine monoclonal antibody (MAb)
 CC 2B6 light chain (see AA42452). It is encoded by a DNA construct
 CC (see AA03497) in vector pCMVILSHZLC1.0 (see AA03504). The humanised
 CC light chain has been expressed in transfected COS host cells. The
 CC invention provides antibodies, especially altered, chimeric and
 CC humanised antibodies which are characterised by hIL-5 specificity,
 CC neutralising activity and affinity for hIL-5. The antibodies are
 CC useful for treating hIL-5-mediated disorders such as asthma,
 CC allergic rhinitis and atopic dermatitis, and can also be used in
 CC the diagnosis of such conditions by measurement (e.g. by ELISA) of
 CC endogenous hIL-5 levels. Also provided are vectors and transformed
 CC host cells for expression of the novel antibodies.
 XX
 SQ Sequence 113 AA:
 XX
 Query Match 43.8%; Score 63; DB 19; Length 113;
 Best Local Similarity 77.8%; Pred. No. 0.29;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 12 SSGGTATAPASSLQAE 29
 DB 71 ssggtatflltislgaed 88
 XX
 RESULT 10
 AAB18857
 ID AAB18857 standard; Protein; 113 AA.
 XX
 AC AAB18857;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of anti-p53 antibody light chain clone 163.2.
 XX
 KM p53; antibody; immune response; vaccine; gene therapy; cancer;
 KM rheumatoid arthritis; coronary heart disease.
 XX
 OS Homo sapiens.
 OS
 PN WO200056770-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-AU00189.
 XX
 PR 19-MAR-1999; 99AU-0009321.
 XX
 PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
 XX
 PI Ward RL, Coomber DWJ;
 XX
 DR WPI: 2000-638249/61.
 DR N-PSDB; AAA96134.
 XX
 PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
 PT fragments, useful in treatment and diagnosis of cancer, rheumatoid

PT arthritis and coronary heart disease -
 XX
 PS Claim 30; Page 132; 163pp; English.
 XX
 CC The present sequence represents the light chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibodies
 CC are useful in pharmaceutical compositions, which additionally contain
 CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
 CC or gadolinium. The polypeptide components of the antibodies are useful in
 CC vaccines, for inducing an immune response against a disease in a
 CC vertebrate, for treatment and/or prophylaxis of disease and for detection
 CC purposes. The nucleic acid sequences can be used to detect a disease as
 CC well as for gene therapy and recombinant production of the polypeptides.
 CC In particular, the following can be treated cancer, rheumatoid arthritis
 CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
 CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
 CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
 CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
 CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
 CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
 XX
 SQ Sequence 113 AA:
 XX
 Query Match 43.8%; Score 63; DB 21; Length 113;
 Best Local Similarity 77.8%; Pred. No. 0.29;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 12 SSGGTATAPASSLQAE 29
 DB 71 ssggtatflltislgaed 88
 XX
 RESULT 11
 AAB18861
 ID AAB18861 standard; Protein; 113 AA.
 XX
 AC AAB18861;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of anti-p53 antibody light chain clone 163.6.
 XX
 KM p53; antibody; immune response; vaccine; gene therapy; cancer;
 KM rheumatoid arthritis; coronary heart disease.
 XX
 OS Homo sapiens.
 OS
 PN WO200056770-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-AU00189.
 XX
 PR 19-MAR-1999; 99AU-0009321.
 XX
 PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
 XX
 PI Ward RL, Coomber DWJ;
 XX
 DR WPI: 2000-638249/61.
 DR N-PSDB; AAA96138.
 XX
 PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
 PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
 PT arthritis and coronary heart disease -
 XX
 PS Claim 30; Page 136; 163pp; English.
 XX
 CC The present sequence represents the light chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibodies

are useful in pharmaceutical compositions, which additionally contain chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA;

Query Match 43.8%; Score 63; DB 21; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSGTAPASSLQAE 29
||||| |
Db 71 ssgsfcltlsslqae 88

RESULT 12
AAB18863
ID AAB18863 standard; Protein: 113 AA.
XX AAB18863;
XX
XX
XX 08-FEB-2001 (first entry)
XX
XX Amino acid sequence of anti-p53 antibody light chain clone 163.7.
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
XX
XX rheumatoid arthritis; coronary heart disease.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FT Misc-difference 101
XX FT /note= "Arg encoded by CCA"
XX PN
XX MO200056770-A1.
XX
XX 28-SEP-2000.
XX PD
XX
XX 15-MAR-2000; 2000WO-AU00189.
XX PF
XX
XX 19-MAR-1999; 99AU-0009321.
XX PR
XX
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX PA
XX Ward RL, Coomber DMJ;
XX PI
XX
XX WPI: 2000-638249/61.
XX DR N-PSDB; AAA96140.
XX
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease
XX PT
XX
XX Claim 30; Page 138; 163pp; English.
XX PS
XX
XX The present sequence represents the light chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA;

Query Match 43.8%; Score 63; DB 21; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSGTAPASSLQAE 29
||||| |
Db 71 ssgsfcltlsslqae 88

RESULT 13
AAB18869
ID AAB18869 standard; Protein: 113 AA.
XX AAB18869;
XX
XX
XX 08-FEB-2001 (first entry)
XX
XX Amino acid sequence of anti-p53 antibody light chain clone 163.15.
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
XX
XX rheumatoid arthritis; coronary heart disease.
XX
XX Homo sapiens.
XX
XX
XX MO200056770-A1.
XX
XX 28-SEP-2000.
XX PD
XX
XX 15-MAR-2000; 2000WO-AU00189.
XX PF
XX
XX 19-MAR-1999; 99AU-0009321.
XX PR
XX
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX PA
XX Ward RL, Coomber DMJ;
XX PI
XX
XX WPI: 2000-638249/61.
XX DR N-PSDB; AAA96146.
XX
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease
XX PT
XX
XX Claim 30; Page 144; 163pp; English.
XX PS
XX
XX The present sequence represents the light chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,

CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
XX
SQ Sequence 113 AA:

Query Match 43.8%; Score 63; DB 21; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSDATAPASSLOAED 29
Db 71 ssgsdftltlslsqaed 88
||||| | |||||

RESULT 14
AAB18871
ID AAB18871 standard; Protein; 113 AA.

XX AAB18871:

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody light chain clone 163.16.

XX p53; antibody; immune response; vaccine; gene therapy; cancer;

KW rheumatoid arthritis; coronary heart disease.

XX Homo sapiens.

PN WO200056770-A1.

XX 28-SEP-2000.

PF 15-MAR-2000; 2000WO-AU00189.

PR 19-MAR-1999; 99AU-0009321.

XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PA Ward RL, Coomber DMU;

DR WPI: 2000-638249/61.

DR N-PSDB; AAA96148.

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide

PT fragments, useful in treatment and diagnosis of cancer, rheumatoid

PT arthritis and coronary heart disease -

XX Claim 30: Page 146; 163pp; English.

CC The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

XX Sequence 113 AA:

Query Match 43.8%; Score 63; DB 21; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSDATAPASSLOAED 29
Db 71 ssgsdftltlslsqaed 88
||||| | |||||

RESULT 15
AAB18873
ID AAB18873 standard; Protein; 113 AA.

XX AAB18873:

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody light chain clone 163.17.

XX p53; antibody; immune response; vaccine; gene therapy; cancer;

KW rheumatoid arthritis; coronary heart disease.

XX Homo sapiens.

PN WO200056770-A1.

XX 28-SEP-2000.

PF 15-MAR-2000; 2000WO-AU00189.

PR 19-MAR-1999; 99AU-0009321.

XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PA Ward RL, Coomber DMU;

DR WPI: 2000-638249/61.

DR N-PSDB; AAA96150.

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide

PT fragments, useful in treatment and diagnosis of cancer, rheumatoid

PT arthritis and coronary heart disease -

XX Claim 30: Page 148; 163pp; English.

CC The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

XX Sequence 113 AA:

Query Match 43.8%; Score 63; DB 21; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSDATAPASSLOAED 29
||||| | |||||

Mon Jul 15, 13:58:19 2002

us-09-712-819a-10.open.rag

Page 9

Db 71 ssgtaftltlsslgad 88

Search completed: July 15, 2002, 12:57:59
Job time: 415 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: July 15, 2002, 12:59:20 ; Search time 75.67 Seconds
(without alignments)
9.361 Million cell updates/sec

Title: US-09-712-819A-10
144
Sequence: 1 YERKKRRQRSSGSGTADAPASSLQAED 29

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/Dackfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	43.8	80	3	US-08-554-840-13 Sequence 13, Appl
2	63	43.8	80	3	US-08-554-840-15 Sequence 15, Appl
3	63	43.8	107	3	US-08-554-840-2 Sequence 2, Appl
4	63	43.8	107	4	US-08-525-539A-81 Sequence 81, Appl
5	63	43.8	112	1	US-07-942-245-30 Sequence 30, Appl
6	63	43.8	113	1	US-08-467-420A-21 Sequence 21, Appl
7	63	43.8	113	1	US-08-470-110A-21 Sequence 21, Appl
8	63	43.8	113	1	US-08-667-769A-21 Sequence 21, Appl
9	63	43.8	113	3	US-08-940-371-21 Sequence 21, Appl
10	63	43.8	113	3	US-08-637-647-21 Sequence 21, Appl
11	63	43.8	113	4	US-08-525-539A-80 Sequence 80, Appl
12	63	43.8	113	5	PCT-US93-08435-6 Sequence 6, Appl
13	63	43.8	113	5	PCT-US93-08435-8 Sequence 8, Appl
14	63	43.8	113	5	PCT-US93-17082A-21 Sequence 21, Appl
15	63	43.8	114	1	US-08-360-125-6 Sequence 6, Appl
16	63	43.8	114	2	US-08-450-578-6 Sequence 6, Appl
17	63	43.8	114	2	US-09-017-628-6 Sequence 6, Appl
18	63	43.8	114	2	US-09-014-880-6 Sequence 6, Appl
19	63	43.8	114	4	US-09-025-769B-17 Sequence 17, Appl
20	63	43.8	115	4	US-09-025-769B-31 Sequence 31, Appl
21	63	43.8	120	1	US-09-025-769B-49 Sequence 49, Appl
22	63	43.8	120	4	US-08-026-320A-4 Sequence 4, Appl
23	63	43.8	127	4	US-08-525-539A-65 Sequence 65, Appl
24	63	43.8	131	2	US-08-483-636-14 Sequence 14, Appl
25	63	43.8	131	2	US-08-483-636-58 Sequence 58, Appl
26	63	43.8	131	2	US-08-483-632-14 Sequence 14, Appl
27	63	43.8	131	2	US-08-483-632-58 Sequence 58, Appl

28	63	43.8	133	3	US-08-463-903-4 Sequence 4, Appl
29	63	43.8	133	4	US-07-935-695-4 Sequence 4, Appl
30	63	43.8	135	3	US-08-812-586-46 Sequence 46, Appl
31	63	43.8	155	3	US-08-828-741B-11 Sequence 11, Appl
32	63	43.8	155	4	US-09-160-567-11 Sequence 11, Appl
33	63	43.8	171	3	US-08-463-903-20 Sequence 20, Appl
34	63	43.8	171	4	US-07-935-695-20 Sequence 20, Appl
35	63	43.8	241	2	US-07-916-098A-56 Sequence 56, Appl
36	63	43.8	260	3	US-08-463-903-2 Sequence 2, Appl
37	63	43.8	260	4	US-07-935-695-2 Sequence 2, Appl
38	63	43.8	275	3	US-08-463-903-6 Sequence 6, Appl
39	63	43.8	285	4	US-07-935-695-6 Sequence 6, Appl
40	63	43.8	285	3	US-08-463-903-22 Sequence 22, Appl
41	63	43.8	285	4	US-07-935-695-22 Sequence 22, Appl
42	63	43.8	342	3	US-08-828-741B-6 Sequence 6, Appl
43	63	43.8	342	4	US-09-160-567-6 Sequence 6, Appl
44	63	43.8	495	3	US-08-828-741B-4 Sequence 4, Appl
45	63	43.8	495	4	US-09-160-567-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-554-840-13
; Sequence 13, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabli
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39.
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Rodin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-554-840-13

Query Match 43.8%; Score 63; DB 3; Length 80;
Best Local Similarity 77.8%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 12 SSGGTADAPASSLQAED 29

Db 47 SSGSTDFTLTSSLOAED 64

RESULT 2

US-08-554-840-15
Sequence 15, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabli
APPLICANT: PADLAN, Eduardo A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22133-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-15

Query Match 43.8%; Score 63; DB 3; Length 80;
Best Local Similarity 77.8%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSTDFTLTSSLOAED 29

Db 47 SSGSTDFTLTSSLOAED 64

RESULT 3
US-08-554-840-2
Sequence 2, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabli
APPLICANT: PADLAN, Eduardo A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404

CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22133-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-2

Query Match 43.8%; Score 63; DB 3; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.041;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSTDFTLTSSLOAED 29

Db 65 SSGSTDFTLTSSLOAED 82

RESULT 4
US-08-525-539A-81
Sequence 81, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO CUTO, FERNANDO J. R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: M31 ANTI-B446 ANTIBODY, METHODS OF USE THEREOF, AND
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-81

Query Match 43.8%; Score 63; DB 4; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.041;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGGTATAPASSLOAED 29
||||| | |||||
DB 65 SSGGTDTLTITSSLOAED 82

RESULT 5
US-07-942-245-30
Sequence 30, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REBS, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUTLD, Bryndon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Suphrue, Mon, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-30

Query Match 43.8%; Score 63; DB 1; Length 112;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGGTATAPASSLOAED 29
||||| | |||||
DB 71 SSGGTDTLTITSSLOAED 88

RESULT 6
US-08-467-420A-21

Sequence 21, Application US/08467420A
Patent No. 5683892
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P. O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,420A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-420A-21

Query Match 43.8%; Score 63; DB 1; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGGTATAPASSLOAED 29
||||| | |||||
DB 71 SSGGTDTLTITSSLOAED 88

RESULT 7
US-08-470-110A-21
Sequence 21, Application US/08470110A
Patent No. 5693323
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.

TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110A
FILING DATE:
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-470-110A-21

Query Match 43.8%; Score 63; DB 1; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGTDPATAPASSIQAE 29
DB 71 SSGTDPFTLTISLQAE 88

RESULT 8
US-08-667-769A-21
Sequence 21, Application US/08667769A
Patent No. 5783184
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,769A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17082
FILING DATE: 22-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50503
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-667-769A-21

Query Match 43.8%; Score 63; DB 1; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGTDPATAPASSIQAE 29
DB 71 SSGTDPFTLTISLQAE 88

RESULT 9
US-08-940-371-21
Sequence 21, Application US/08940371
Patent No. 5851525
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,371
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110
FILING DATE:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5090
TELEFAX: 610 270-5024
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-940-371-21

Query Match 43.8%; Score 63; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGGTDTAPASSLOAED 29
||||| |
Db 71 SSGGTDTFTLTISSLOAED 88

RESULT 10
US-08-637-647-21
Sequence 21, Application US/08637647
Patent No. 6129913
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,647
FILING DATE: 19-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/363,131
FILING DATE:
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5090
TELEFAX: 610 270-5024
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-637-647-21

Query Match 43.8%; Score 63; DB 3; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGGTDTAPASSLOAED 29
||||| |
Db 71 SSGGTDTFTLTISSLOAED 88

RESULT 11
US-08-525-539A-80
Sequence 80, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-80

Query Match 43.8%; Score 63; DB 4; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSGDTAPASSLOAED 29
||||| | |||||
Db 71 SSGSGDTFTLTSSLOAED 88

RESULT 12
PCT-US93-08435-6
; Sequence 6, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Conferring Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-08435-6

Query Match 43.8%; Score 63; DB 5; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSGDTAPASSLOAED 29
||||| | |||||
Db 71 SSGSGDTFTLTSSLOAED 88

RESULT 13
PCT-US93-08435-8
; Sequence 8, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Conferring Passive

; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-08435-8

Query Match 43.8%; Score 63; DB 5; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSGDTAPASSLOAED 29
||||| | |||||
Db 71 SSGSGDTFTLTSSLOAED 88

RESULT 14
PCT-US95-17082a-21
; Sequence 21, Application PC/TUS9517082a
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UM2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/17082A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/470110
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/467420
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/363131
;; FILING DATE: 23-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sutton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50282-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5024
;; TELEFAX: 610-270-5090
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US95-17082A-21

Query Match 43.8%; Score 63; DB 5; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 12 SSGSGDATAPASSLOAED 29
||||| |
Db 71 SSGSGDFTLTITSSLOAED 88

RESULT 15
US-08-360-125-6
; Sequence 6, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiko NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Menderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 Inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 42A
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX:
;; INDEX:
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE: Hybridoma producing human
;; CELL LINE: antibody GAH
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-6

Query Match 43.8%; Score 63; DB 1; Length 114;
Best Local Similarity 77.8%; Pred. No. 0.044;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 12 SSGSGDATAPASSLOAED 29
||||| |
Db 71 SSGSGDFTLTITSSLOAED 88

Search completed: July 15, 2002, 12:59:20
Job time: 391 sec

